

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Gaugler, Béatrice; Van den Eynde, Benoît;
van der Bruggen, Pierre; Boon-Falleur, Thierry
- (ii) TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Felfe & Lynch
(B) STREET: 805 Third Avenue
(C) CITY: New York City
(D) STATE: New York
(F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
(B) COMPUTER: IBM
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/037,230
(B) FILING DATE: 26-MARCH-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US92/04354
(B) FILING DATE: 22-MAY-1992
- (viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/807,043
(B) FILING DATE: 12-DECEMBER-1991
- (ix) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/764,364
(B) FILING DATE: 23-SEPTEMBER-1991
- (x) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/728,838
(b) FILING DATE: 9-JULY-1991
- (xi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/705,702
(B) FILING DATE: 23-MAY-1991
- (xii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Hanson, Norman D.
(B) REGISTRATION NUMBER: 30,946
(C) REFERENCE/DOCKET NUMBER: LUD 253.5
- (xiii) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 688-9200
(B) TELEFAX: (212) 838-3884

009250-4543-052600

- (2) INFORMATION FOR SEQUENCE ID NO: 1:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 462 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60
ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT 120
CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTCGA AGTTCCGCCT ACAGCTCTAG 180
CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240
CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG CATGCATTGT 360
GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT 420
TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC 462

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(2) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG	TCT	GAT	AAC	AAG	AAA	CCA	GAC	AAA	GCC	CAC	AGT	GGC	TCA	GGT	GGT	48
Met	Ser	Asp	Asn	Lys	Lys	Pro	Asp	Lys	Ala	His	Ser	Gly	Ser	Gly	Gly	
				5					10					15		
GAC	GGT	GAT	GGG	AAT	AGG	TGC	AAT	TTA	TTG	CAC	CGG	TAC	TCC	CTG	GAA	96
Asp	Gly	Asp	Gly	Asn	Arg	Cys	Asn	Leu	Leu	His	Arg	Tyr	Ser	Leu	Glu	
			20					25					30			
GAA	ATT	CTG	CCT	TAT	CTA	GGG	TGG	CTG	GTC	TTC	GCT	GTT	GTC	ACA	ACA	144
Glu	Ile	Leu	Pro	Tyr	Leu	Gly	Trp	Leu	Val	Phe	Ala	Val	Val	Thr	Thr	
		35					40					45				
AGT	TTT	CTG	GCG	CTC	CAG	ATG	TTC	ATA	GAC	GCC	CTT	TAT	GAG	GAG	CAG	192
Ser	Phe	Leu	Ala	Leu	Gln	Met	Phe	Ile	Asp	Ala	Leu	Tyr	Glu	Glu	Gln	
	50				55				60							
TAT	GAA	AGG	GAT	GTG	GCC	TGG	ATA	GCC	AGG	CAA	AGC	AAG	CGC	ATG	TCC	240
Tyr	Glu	Arg	Asp	Val	Ala	Trp	Ile	Ala	Arg	Gln	Ser	Lys	Arg	Met	Ser	
	65			70					75					80		
TCT	GTC	GAT	GAG	GAT	GAA	GAC	GAT	GAG	GAT	GAT	GAG	GAT	GAC	TAC	TAC	288
Ser	Val	Asp	Glu	Asp	Glu	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Asp	Tyr	Tyr	
			85					90					95			
GAC	GAC	GAG	GAC	GAC	GAC	GAC	GAT	GCC	TTC	TAT	GAT	GAT	GAG	GAT	GAT	336
Asp	Asp	Glu	Asp	Asp	Asp	Asp	Asp	Ala	Phe	Tyr	Asp	Asp	Glu	Asp	Asp	
		100						105					110			
GAG	GAA	GAA	GAA	TTG	GAG	AAC	CTG	ATG	GAT	GAT	GAA	TCA	GAA	GAT	GAG	384
Glu	Glu	Glu	Glu	Leu	Glu	Asn	Leu	Met	Asp	Asp	Glu	Ser	Glu	Asp	Glu	
		115					120					125				
GCC	GAA	GAA	GAG	ATG	AGC	GTG	GAA	ATG	GGT	GCC	GGA	GCT	GAG	GAA	ATG	432
Ala	Glu	Glu	Glu	Met	Ser	Val	Glu	Met	Gly	Ala	Gly	Ala	Glu	Glu	Met	
	130					135					140					
GGT	GCT	GGC	GCT	AAC	TGT	GCC	TGT	GTT	CCT	GGC	CAT	CAT	TTA	AGG	AAG	480
Gly	Ala	Gly	Ala	Asn	Cys	Ala	Cys	Val	Pro	Gly	His	His	Leu	Arg	Lys	
	145			150						155				160		
AAT	GAA	GTG	AAG	TGT	AGG	ATG	ATT	TAT	TTC	TTC	CAC	GAC	CCT	AAT	TTC	528
Asn	Glu	Val	Lys	Cys	Arg	Met	Ile	Tyr	Phe	Phe	His	Asp	Pro	Asn	Phe	
			165					170					175			
CTG	GTG	TCT	ATA	CCA	GTG	AAC	CCT	AAG	GAA	CAA	ATG	GAG	TGT	AGG	TGT	576
Leu	Val	Ser	Ile	Pro	Val	Asn	Pro	Lys	Glu	Gln	Met	Glu	Cys	Arg	Cys	
		180					185						190			
GAA	AAT	GCT	GAT	GAA	GAG	GTT	GCA	ATG	GAA	GAG	GAA	GAA	GAA	GAA	GAG	624
Glu	Asn	Ala	Asp	Glu	Glu	Val	Ala	Met	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
		195					200				210					
GAG	GAG	GAG	GAG	GAA	GAG	GAA	ATG	GGA	AAC	CCG	GAT	GGC	TTC	TCA	CCT	672
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Met	Gly	Asn	Pro	Asp	Gly	Phe	Ser	Pro	
	220				225				230					235		
TAG																675

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- (2) INFORMATION FOR SEQUENCE ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCATGCAGTT	GCAAAGCCCA	GAAGAAAGAA	ATGGACAGCG	GAAGAAGTGG	TTGTTTTTTT	60
TTCCCCTTCA	TTAATTTTCT	AGTTTTTAGT	AATCCAGAAA	ATTTGATTTT	GTTCTAAAGT	120
TCATTATGCA	AAGATGTCAC	CAACAGACTT	CTGACTGCAT	GGTGAACTTT	CATATGATAC	180
ATAGGATTAC	ACTTGTACCT	GTTAAAAATA	AAAGTTTGAC	TTGCATAC		228

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- (2) INFORMATION FOR SEQUENCE ID NO: 4:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1365 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG	AATGAAAAGA	ACCCGGGACT	CCCAAAGACG	CTAGATGTGT	50
GAAGATCCTG	ATCACTCATT	GGGTGTCTGA	GTTCTGCGAT	ATTTCATCCCT	100
CAGCCAATGA	GCTTACTGTT	CTCGTGGGGG	GTTTGTGAGC	CTTGGGTAGG	150
AAGTTTTGCA	AGTTCCGCCT	ACAGCTCTAG	CTTGTGAATT	TGTACCCTTT	200
CACGTAAAAA	AGTAGTCCAG	AGTTTACTAC	ACCCTCCCTC	CCCCCTCCCA	250
CCTCGTGCTG	TGCTGAGTTT	AGAAGTCTTC	CTTATAGAAG	TCTTCCGTAT	300
AGAACTCTTC	CGGAGGAAGG	AGGGAGGACC	CCCCCCTTTT	GCTCTCCCAG	350
CATGCATTGT	GTCAACGCCA	TTGCACTGAG	CTGGTCGAAG	AAGTAAGCCG	400
CTAGCTTGCG	ACTCTACTCT	TATCTTAACT	TAGCTCGGCT	TCCTGCTGGT	450
ACCCTTTGTG	CC				462
ATG TCT GAT	AAC AAG AAA CCA GAC	AAA GCC CAC	AGT GGC TCA		504
GGT GGT GAC	GGT GAT GGG AAT AGG	TGC AAT TTA	TTG CAC CGG		546
TAC TCC CTG	GAA GAA ATT CTG	CCT TAT CTA	GGG TGG CTG	GTC	588
TTC GCT GTT	GTC ACA ACA AGT	TTT CTG GCG	CTC CAG ATG	TTC	630
ATA GAC GCC	CTT TAT GAG GAG	CAG TAT GAA	AGG GAT GTG	GCC	672
TGG ATA GCC	AGG CAA AGC AAG	CGC ATG TCC	TCT GTC GAT	GAG	714
GAT GAA GAC	GAT GAG GAT GAT	GAG GAT GAC	TAC TAC GAC	GAC	756
GAG GAC GAC	GAC GAC GAT GCC	TTC TAT GAT	GAT GAG GAT	GAT	798
GAG GAA GAA	GAA TTG GAG AAC	CTG ATG GAT	GAT GAA TCA	GAA	840
GAT GAG GCC	GAA GAA GAG ATG	AGC GTG GAA	ATG GGT GCC	GGA	882
GCT GAG GAA	ATG GGT GCT GGC	GCT AAC TGT	GCC TGT GTT	CCT	924
GGC CAT CAT	TTA AGG AAG AAT	GAA GTG AAG	TGT AGG ATG	ATT	966
TAT TTC TTC	CAC GAC CCT AAT	TTC CTG GTG	TCT ATA CCA	GTG	1008
AAC CCT AAG	GAA CAA ATG GAG	TGT AGG TGT	GAA AAT GCT	GAT	1050
GAA GAG GTT	GCA ATG GAA GAG	GAA GAA GAA	GAG GAG GAG		1092
GAG GAG GAA	GAG GAA ATG GGA	AAC CCG GAT	GGC TTC TCA	CCT	1134
TAG					1137
GCATGCAGTT	GCAAAGCCCA	GAAGAAAGAA	ATGGACAGCG	GAAGAAGTGG	1187
TTGTTTTTTT	TTCCCCTTCA	TTAATTTTCT	AGTTTTTGT	AATCCAGAAA	1237
ATTTGATTTT	GTTCTAAAGT	TCATTATGCA	AAGATGTCAC	CAACAGACTT	1287
CTGACTGCAT	GGTGAACCTT	CATATGATAC	ATAGGATTAC	ACTTGTACCT	1337
GTAAAAATA	AAAGTTTGAC	TTGCATAC			1365

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- (2) INFORMATION FOR SEQUENCE ID NO: 5:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4698 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACCACAGGAG AATGAAAAGA ACCCGGGGACT CCCAAAGACG CTAGATGTGT 50
 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100
 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
 AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200
 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG 350
 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
 ACCCTTTGTG CC 462
 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756
 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T 916
 GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA 966
 CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC 1016
 TGGAGCCATT CTTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC 1066
 CCCCACCTCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC 1116
 TTCAGTCCAT CTGTCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC 1166
 TCCCCCTCGG CTCAACTTTT CGTGCCCTTCT GCTCTCTGAT CCCCACCCTC 1216
 TTCAGGCTTC CCCATTTGCT CCTCTCCCCA AACCCTCCCC TTCTGTTC 1266
 CCTTTTCGCG CCTTTTCTTT CTTGCTCCCC TCCCCCTCCC TATTTACCTT 1316
 TCACCAGCTT TGCTCTCCCT GCTCCCCCTC CCCTTTTGCA CCTTTTCTTT 1366
 TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCTT 1416
 CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG 1466
 TGCTCTCTCC TCCCCCTCCC CCTCCCCCTT TATTTGCATT TTCGGGTGCT 1516
 CCTCCCCCTC CTCCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT 1566
 TTGGTTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GTCTGGCAC 1616
 TCACTCTGTA GACCAGGCTG GCCTCAAACCT CAGAAATCTG CCTGCCTCTG 1666
 CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG 1716
 GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT 1766
 AACTCCCCCT TTGGCACCTT TCCTTTACAG GACCCCTCC CCCTCCCTGT 1816
 TTCCCTTCCG GCACCCTTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC 1866
 CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CCTGCTTTCT 1916
 GCCCGTTTCC CTTTTTTTGT GCCTTTCCTC CTGGCTCCCC TCCACCTTCC 1966
 AGCTCACCTT TTTGTTTGTT TGGTTGTTTG GTTGTGTTGGT TTGCTTTTTT 2016
 TTTTTTTTTT GCACCTTGTT TTCCAAGATC CCCCTCCCCC TCCGGCTTCC 2066
 CCTCTGTGTG CTTTTCCTGT TCCCTCCCCC TCGCTGGCTC CCCCTCCCTT 2116
 TCTGCCTTTC CTGTCCCTGC TCCCTTCTCT GCTAACCTTT TAATGCCTTT 2166
 CTTTCTAGA CTCCCCCTC CAGGCTTGCT GTTTGCTTCT GTGCACTTTT 2216
 CCTGACCCTG CTCCCCCTCC CCTCCAGCT CCCCCCTCTT TTCCCACCTC 2266
 CCTTTCTCCA GCCTGTCACC CCTCCTTCTC TCCTCTCTGT TTCTCCCACT 2316
 TCCTGCTTCC TTTACCCCTT CCTCTCCTC ACTCTCCTCC CTGCCTGCTG 2366
 GACTTCTCTT CCAGCCGCCC AGTTCCCTGC AGTCTGGAG TCTTTCCTGC 2416
 CTCTCTGTCT CTACTTCCC CTTAGTTTCA CTTCCCTTTC ACTCTCCCT 2466
 ATGTGTCTCT CTTCTATCT ATCCCTTCC TTTCTGTCCT TCTCCTCTGT 2516
 CCATCACCTC TCTCCTCCCT TCCCTTTCCT CTCTCTTCCA TTTTCTTCCA 2566
 CCTGCTTCTT TACCCTGCCT CTCCCATTGC CCTCTTACCT TTATGCCCAT 2616
 TCCATGTCCC CTCTCAATTC CCTGTCCCAT TGTGCTCCCT CACATCTTCC 2666

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ATTTCCCTCT	TTCTCCCTTA	GCCTCTTCTT	CCTCTTCTCT	TGTATCTCCC	2716
TTCCCTTTGC	TTCTCCCTCC	TCCTTTCCCC	TTCCCTATAG	CCCTCTACTC	2766
TACTTGATCT	TCTCTCCTCT	CCACATACCC	TTTTTCCTTT	CCACCCTGCC	2816
CTTTGTCCCC	AGACCCTACA	GTATCCTGTG	CACAGGAAGT	GGGAGGTGCC	2866
ATCAACAACA	AGGAGGCAAG	AAACAGAGCA	AAATCCCAAA	ATCAGCAGGA	2916
AAGGCTGGAT	GAAAATAAGG	CCAGGTTCTG	AGGACAGCTG	GAATCTAGCC	2966
AAGTGGCTCC	TATAACCCTA	AGTACCAAGG	GAGAAAAGTGA	TGGTGAAGTT	3016
CTTGATCCTT	GCTGCTTCTT	TTACATATGT	TGGCACATCT	TTCTCAAATG	3066
CAGGCCATGC	TCCATGCTTG	GCGCTTGCTC	AGCGTGGTTA	AGTAATGGGA	3116
GAATCTGAAA	ACTAGGGGCC	AGTGGTTTGT	TTTGGGGACA	AATTAGCACG	3166
TAGTGATATT	TCCCCCTAAA	AATTATAACA	AACAGATTCA	TGATTTGAGA	3216
TCCTTCTACA	GGTGAGAAGT	GGAAAAATTG	TCACTATGAA	GTTCTTTTAA	3266
GGCTAAAGAT	ACTTGGAACC	ATAGAAGCGT	TGTTAAAATA	CTGCTTTCTT	3316
TTGCTAAAAT	ATTCTTTCTC	ACATATTTCAT	ATTCTCCAG		3355
GT GTT CCT	GGC CAT CAT	TTA AGG AAG	AAT GAA GTG	AAG TGT	3396
AGG ATG ATT	TAT TTC TTC	CAC GAC CCT	AAT TTC CTG	GTG TCT	3438
ATA CCA GTG	AAC CCT AAG	GAA CAA ATG	GAG TGT AGG	TGT GAA	3480
AAT GCT GAT	GAA GAG GTT	GCA ATG GAA	GAG GAA GAA	GAA GAA	3522
GAG GAG GAG	GAG GAG GAA	GAG GAA ATG	GGA AAC CCG	GAT GGC	3564
TTC TCA CCT	TAG				3576
GCATGCAGGT	ACTGGCTTCA	CTAACCAACC	ATTCCTAACA	TATGCCTGTA	3626
GCTAAGAGCA	TCTTTTTTAAA	AAATATTATT	GGTAAACTAA	ACAATTGTTA	3676
TCTTTTTTACA	TTAATAAGTA	TTAAATTAAT	CCAGTATACA	GTTTTAAGAA	3726
CCCTAAGTTA	AACAGAAGTC	AATGATGTCT	AGATGCCTGT	TCTTTAGATT	3776
GTAGTGAGAC	TACTTACTAC	AGATGAGAAG	TTGTTAGACT	CGGGAGTAGA	3826
GACCAGTAAA	AGATCATGCA	GTGAAATGTG	GCCATGGAAA	TCGCATATTG	3876
TTCTTATAGT	ACCTTTGAGA	CAGCTGATAA	CAGCTGACAA	AAATAAGTGT	3926
TTCAAGAAAAG	ATCACACGCC	ATGGTTCACA	TGCAAATTAT	TATTTTGTCG	3976
TTCTGATTTT	TTTCATTTCT	AGACCTGTGG	TTTTAAAGAG	ATGAAAATCT	4026
CTTAAAATTT	CCTTCATCTT	TAATTTTCCT	TACTTTTAGT	TTTTTTCACT	4076
TAGAATTCAA	TTCAAATTCT	TAATTCAATC	TTAATTTTTA	GATTTCTTAA	4126
AATGTTTTTT	AAAAAAAATG	CAAATCTCAT	TTTTAAGAGA	TGAAAGCAGA	4176
GTAACCTGGGG	GGCTTAGGGG	ATCTGTAGGG	TTGCGGTATA	GCAATAGGGA	4226
GTTCTGGTCT	CTGAGAAGCA	GTCAGAGAGA	ATGGAAAACC	AGGCCCTTGC	4276
CAGTAGGTTA	GTGAGGTTGA	TATGATCAGA	TTATGGACAC	TCTCCAAATC	4326
ATAAATACTC	TAACAGCTAA	GGATCTCTGA	GGGAAACACA	ACAGGGAAAT	4376
ATTTTAGTTT	CTCCTTGAGA	AACAATGACA	AGACATAAAA	TTGGCAAGAA	4426
AGTCAGGAGT	GTATTCTAAT	AAGTGTTGCT	TATCTCTTAT	TTTCTTCTAC	4476
AGTTGCAAAG	CCCAGAAGAA	AGAAATGGAC	AGCGGAAGAA	GTGGTTGTTT	4526
TTTTTTCCCC	TTCAATTAATT	TTCTAGTTTT	TAGTAATCCA	GAAAATTTGA	4576
TTTTGTCTTA	AAGTTCATTA	TGCAAAGATG	TCACCAACAG	ACTTCTGACT	4626
GCATGGTGAA	CTTTCATATG	ATACATAGGA	TTACACTTGT	ACCTGTTAAA	4676
AATAAAAGTT	TGACTTGCAT	AC			4698

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- (2) INFORMATION FOR SEQUENCE ID NO: 6:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu Val Phe
5

003250" E4562560

- (2) INFORMATION FOR SEQUENCE ID NO: 7:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2418 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC	CCTGCCAGGA	AAAATATAAG	GGCCCTGCGT	GAGAACAGAG	50
GGGGTCATCC	ACTGCATGAG	AGTGGGGGATG	TCACAGAGTC	CAGCCCACCC	100
TCCTGGTAGC	ACTGAGAAGC	CAGGGCTGTG	CTTGCGGTCT	GCACCCTGAG	150
GGCCCGTGGA	TTCCTCTTCC	TGGAGCTCCA	GGAACCAGGC	AGTGAGGCCT	200
TGGTCTGAGA	CAGTATCCTC	AGGTCACAGA	GCAGAGGATG	CACAGGGTGT	250
GCCAGCAGTG	AATGTTTGCC	CTGAATGCAC	ACCAAGGGCC	CCACCTGCCA	300
CAGGACACAT	AGGACTCCAC	AGAGTCTGGC	CTCACCTCCC	TACTGTCACT	350
CCTGTAGAAT	CGACCTCTGC	TGGCCGGCTG	TACCCTGAGT	ACCCTCTCAC	400
TTCCTCCTTC	AGGTTTTTCAG	GGGACAGGCC	AACCCAGAGG	ACAGGATTCC	450
CTGGAGGCCA	CAGAGGAGCA	CCAAGGAGAA	GATCTGTAAG	TAGGCCTTTG	500
TTAGAGTCTC	CAAGGTTTCAG	TTCTCAGCTG	AGGCCTCTCA	CACACTCCCT	550
CTCTCCCCAG	GCCTGTGGGT	CTTCATTGCC	CAGCTCCTGC	CCACACTCCT	600
GCCTGCTGCC	CTGACGAGAG	TCATCATGTC	TCTTGAGCAG	AGGAGTCTGC	650
ACTGCAAGCC	TGAGGAAGCC	CTTGAGGCC	AACAAGAGGC	CCTGGGCCTG	700
GTGTGTGTGC	AGGCTGCCAC	CTCCTCCTCC	TCTCCTCTGG	TCCTGGGCAC	750
CCTGGAGGAG	GTGCCCCTG	CTGGGTCAAC	AGATCCTCCC	CAGAGTCCTC	800
AGGGAGCCTC	CGCCTTTCCC	ACTACCATCA	ACTTCACTCG	ACAGAGGCAA	850
CCCAGTGAGG	GTTCCAGCAG	CCGTGAAGAG	GAGGGGCCAA	GCACCTCTTG	900
TATCCTGGAG	TCCTTGTTCC	GAGCAGTAAT	CACCTAAGAAG	GTGGCTGATT	950
TGGTTGGTTT	TCTGCTCCTC	AAATATCGAG	CCAGGGAGCC	AGTCACAAAG	1000
GCAGAAATGC	TGGAGAGTGT	CATCAAAAAT	TACAAGCACT	GTTTTTCCTGA	1050
GATCTTCGGC	AAAGCCTCTG	AGTCCTTGCA	GCTGGTCTTT	GGCATTGACG	1100
TGAAGGAAGC	AGACCCCACC	GGCCACTCCT	ATGTCCTTGT	CACCTGCCTA	1150
GGTCTCTCCT	ATGATGGCCT	GCTGGGTGAT	AATCAGATCA	TGCCCAAGAC	1200
AGGCTTCCTG	ATAATTGTCC	TGGTCATGAT	TGCAATGGAG	GGCGGCCATG	1250
CTCCTGAGGA	GGAAATCTGG	GAGGAGCTGA	GTGTGATGGA	GGTGTATGAT	1300
GGGAGGGAGC	ACAGTGCCTA	TGGGGAGCCC	AGGAAGCTGC	TCACCCAAGA	1350
TTTGTTGTCAG	GAAAAGTACC	TGGAGTACGG	CAGGTGCCCG	ACAGTGATCC	1400
CGCACGCTAT	GAGTTCCTGT	GGGGTCCAAG	GGCCCTCGCT	GAAACCAGCT	1450
ATGTGAAAGT	CCTTGAGTAT	GTGATCAAGG	TCAGTGCAAG	AGTTCGCTTT	1500
TTCTTCCCAT	CCCTGCGTGA	AGCAGCTTTG	AGAGAGGAGG	AAGAGGGAGT	1550
CTGAGCATGA	GTTGCAGCCA	AGGCCAGTGG	GAGGGGGACT	GGGCCAGTGC	1600
ACCTTCCAGG	GCCGCGTCCA	GCAGCTTTCC	CTGCCTCGTG	TGACATGAGG	1650
CCCATTCTTC	ACTCTGAAGA	GAGCGGTCAG	TGTTCTCAGT	AGTAGGTTTC	1700
TGTTCTATTG	GGTGACTTGG	AGATTTATCT	TTGTTCTCTT	TTGGAATTGT	1750
TCAAATGTTT	TTTTTTAAGG	GATGGTTGAA	TGAACCTTCAG	CATCCAAGTT	1800
TATGAATGAC	AGCAGTCACA	CAGTTCTGTG	TATATAGTTT	AAGGGTAAGA	1850
GTCTTGTTGT	TTATTGAGAT	TGGGAAATCC	ATTCTATTTT	GTGAATTGGG	1900
ATAATAACAG	CAGTGGAATA	AGTACTTAGA	AATGTGAAAA	ATGAGCAGTA	1950
AAATAGATGA	GATAAAGAAC	TAAAGAAATT	AAGAGATAGT	CAATTCTTGC	2000
CTTATACCTC	AGTCTATTCT	GTAAAAATTT	TAAAGATATA	TGCATACCTG	2050
GATTTTCCTG	GCTTCTTTGA	GAATGTAAGA	GAAATTAAAT	CTGAATAAAG	2100
AATTCTTCCT	GTTCACTGGC	TCTTTTCTTC	TCCATGCACT	GAGCATCTGC	2150
TTTTTGGGAA	GCCCTGGGTT	AGTAGTGGAG	ATGCTAAGGT	AAGCCAGACT	2200
CATACCCACC	CATAGGGTCG	TAGAGTCTAG	GAGCTGCAGT	CACGTAATCG	2250
AGGTGGCAAG	ATGTCCTCTA	AAGATGTAGG	GAAAAGTGAG	AGAGGGGTGA	2300
GGGTGTGGGG	CTCCGGGTGA	GAGTGGTGGG	GTGTCAATGC	CCTGAGCTGG	2350
GGCATTTTGG	GCTTTGGGAA	ACTGCAGTTC	CTTCTGGGGG	AGCTGATTGT	2400
AATGATCTTG	GGTGGATCC				2418

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- (2) INFORMATION FOR SEQUENCE ID NO: 8:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5724 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-1 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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CCCCGGGGCACC	CACTGGGCATC	CCTCCCCCCTA	CCACCCCCCAA	TCCCTCCCTT	50
TACGCCACCC	ATCCAAACAT	CTTCACGCTC	ACCCCCAGCC	CAAGCCAGGC	100
AGAATCCGGT	TCCACCCCTG	CTCTCAACCC	AGGGAAGCCC	AGGTGCCCAG	150
ATGTGACGCC	ACTGACTTGA	GCATTAGTGG	TTAGAGAGAA	GCGAGGTTTT	200
CGGTCTGAGG	GGCGGCTTGA	GATCGGTGGA	GGGAAGCGGG	CCCAGCTCTG	250
TAAGGAGGCA	AGGTGACATG	CTGAGGGAGG	ACTGAGGACC	CACTTACCCC	300
AGATAGAGGA	CCCCAAATAA	TCCCTTCATG	CCAGTCCTGG	ACCATCTGGT	350
GGTGGACTTC	TCAGGCTGGG	CCACCCCCAG	CCCCCTTGCT	GCTTAAACCA	400
CTGGGGACTC	GAAGTCAGAG	CTCCGTGTGA	TCAGGGAAGG	GCTGCTTAGG	450
AGAGGGCAGC	GTCCAGGCTC	TGCCAGACAT	CATGCTCAGG	ATTCTCAAGG	500
AGGGCTGAGG	GTCCCTAAGA	CCCCACTCCC	GTGACCCAAC	CCCCACTCCA	550
ATGCTCACTC	CCGTGACCCA	ACCCCTCTTT	CATTGTCAAT	CCAACCCCCA	600
CCCCACATCC	CCCACCCCAT	CCCTCAACCC	TGATGCCCAT	CCGCCCAGCC	650
ATTCCACCCT	CACCCCCACC	CCCACCCCCA	CGCCCACTCC	CACCCCCACC	700
CAGGCAGGAT	CCGGTTCCCG	CCAGGAAACA	TCCGGGTGCC	CGGATGTGAC	750
GCCACTGACT	TGCGCATTGT	GGGGCAGAGA	GAAGCGAGGT	TTCCATTCTG	800
AGGGACGGCG	TAGAGTTCGG	CCGAAGGAAC	CTGACCCAGG	CTCTGTGAGG	850
AGGCAAGGTG	AGAGGCTGAG	GGAGGACTGA	GGACCCCGCC	ACTCCAAATA	900
GAGAGCCCCA	AATATTCCAG	CCCCGCCCTT	GCTGCCAGCC	CTGGCCCCACC	950
CGCGGGAAGA	CGTCTCAGCC	TGGGCTGCCC	CCAGACCCCT	GCTCCAAAAG	1000
CCTTGAGAGA	CACCAGGTTT	TTCTCCCCAA	GCTCTGGAAT	CAGAGGTTGC	1050
TGTGACCAGG	GCAGGACTGG	TTAGGAGAGG	GCAGGGCACA	GGCTCTGCCA	1100
GGCATCAAGA	TCAGCACCCA	AGAGGGAGGG	CTGTGGGCCC	CCAAGACTGC	1150
ACTCCAATCC	CCACTCCCAC	CCCATTCGCA	TTCCCATTC	CCACCCAACC	1200
CCCATCTCCT	CAGCTACACC	TCCACCCCCA	TCCCTACTCC	TACTCCGTCA	1250
CTTGACCACC	ACCCTCCAGC	CCCAGCACCA	CCCCCAACCC	TTCTGCCACC	1300
TCACCCTCAC	TGCCCCCAAC	CCCACCCTCA	TCTCTCTCAT	GTGCCCCACT	1350
CCCATCGCCT	CCCCCATTTT	GGCAGAATCC	GGTTTGCCCC	TGCTCTCAAC	1400
CCAGGGAAGC	CCTGGTAGGC	CCGATGTGAA	ACCCTGACT	TGAACCTCAC	1450
AGATCTGAGA	GAAGCCAGGT	TCATTTAATG	GTTCTGAGGG	GCGGCTTGAG	1500
ATCCACTGAG	GGGAGTGGTT	TTAGGCTCTG	TGAGGAGGCA	AGGTGAGATG	1550
CTGAGGGAGG	ACTGAGGAGG	CACACACCCC	AGGTAGATGG	CCCCAAAATG	1600
ATCCAGTACC	ACCCTGCTG	CCAGCCCTGG	ACCACCCGGC	CAGGACAGAT	1650
GTCTCAGCTG	GACCACCCCC	CGTCCCCTCC	CACTGCCACT	TAACCCACAG	1700
GGCAATCTGT	AGTCATAGCT	TATGTGACCG	GGGCAGGGTT	GGTCAGGAGA	1750
GGCAGGGCCC	AGGCATCAAG	GTCCAGCATC	CGCCCGGCAT	TAGGGTCAGG	1800
ACCCTGGGAG	GGAAGTGAAG	GTTCCCCACC	CACACCTGTC	TCCTCATCTC	1850
CACCGCCACC	CCACTCACAT	TCCCATACCT	ACCCCTTACC	CCCAACCTCA	1900
TCTTGTCAGA	ATCCCTGCTG	TCAACCCACG	GAAGCCACGG	GAATGGCGGC	1950
CAGGCACTCG	GATCTTGACG	TCCCCATCCA	GGGTCTGATG	GAGGGAAGGG	2000
GCTTGAACAG	GGCCTCAGGG	GAGCAGAGGG	AGGGCCCTAC	TGCGAGATGA	2050
GGGAGGCCTC	AGAGGACCCA	GCACCCTAGG	ACACCGCACC	CCTGTCTGAG	2100
ACTGAGGCTG	CCACTTCTGG	CCTCAAGAAT	CAGAACGATG	GGGACTCAGA	2150
TTGCATGGGG	GTGGGACCCA	GGCCTGCAAG	GCTTACGCGG	AGGAAGAGGA	2200
GGGAGGACTC	AGGGGACCTT	GGAATCCAGA	TCAGTGTGGA	CCTCGGCCCT	2250
GAGAGGTCCA	GGGCACGGTG	GCCACATATG	GCCCATATTT	CCTGCATCTT	2300
TGAGGTGACA	GGACAGAGCT	GTGGTCTGAG	AAGTGGGGCC	TCAGGTCAAC	2350
AGAGGGAGGA	GTTCCAGGAT	CCATATGGCC	CAAGATGTGC	CCCCTTCATG	2400
AGGACTGGGG	ATATCCCCGG	CTCAGAAAGA	AGGGACTCCA	CACAGTCTGG	2450
CTGTCCCCTT	TTAGTAGCTC	TAGGGGGGACC	AGATCAGGGA	TGGCGGTATG	2500
TTCCATTCTC	ACTTGTACCA	CAGGCAGGAA	GTTGGGGGGC	CCTCAGGGAG	2550
ATGGGGTCTT	GGGGTAAAGG	GGGGATGTCT	ACTCATGTCA	GGGAATTGGG	2600
GTTTGAGGAA	GCACAGGCGC	TGGCAGGAAT	AAAGATGAGT	GAGACAGACA	2650
AGGCTATTGG	AATCCACACC	CCAGAACCAA	AGGGGTGAGC	CCTGGACACC	2700

TCACCCAGGA	TGTGGCTTCT	TTTTCACTCC	TGTTTCCAGA	TCTGGGGCAG	2750
GTGAGGACCT	CATTCTCAGA	GGGTGACTCA	GGTCAACGTA	GGGACCCCCA	2800
TCTGGTCTAA	AGACAGAGCG	GTCCCAGGAT	CTGCCATGCG	TTCGGGTGAG	2850
GAACATGAGG	GAGGACTGAG	GGTACCCAG	GACCAGAACA	CTGAGGGAGA	2900
CTGCACAGAA	ATCAGCCCTG	CCCCTGCTGT	CACCCCAGAG	AGCATGGGCT	2950
GGGCCGTCTG	CCGAGGTCCT	TCCGTTATCC	TGGGATCATT	GATGTCAGGG	3000
ACGGGGAGGC	CTTGGTCTGA	GAAGGCTGCG	CTCAGGTCAG	TAGAGGGAGC	3050
GTCCCAGGCC	CTGCCAGGAG	TCAAGGTGAG	GACCAAGCGG	GCACCTCACC	3150
CAGGACACAT	TAATTCCAAT	GAATTTTGAT	ATCTCTTGCT	GCCCTTCCCC	3200
AAGGACCTAG	GCACGTGTGG	CCAGATGTTT	GTCCCTCCT	GTCCCTCCAT	3250
TCCTTATCAT	GGATGTGAAC	TCTTGATTTG	GATTTCTCAG	ACCAGCAAAA	3300
GGGCAGGATC	CAGGCCCTGC	CAGGAAAAAT	ATAAGGGCCC	TGCGTGAGAA	3350
CAGAGGGGGT	CATCCACTGC	ATGAGAGTGG	GGATGTACAC	GAGTCCAGCC	3400
CACCCCTCTG	GTAGCACTGA	GAAGCCAGGG	CTGTGCTTGC	GGTCTGCACC	3450
CTGAGGGCCC	GTGGATTCCCT	CTTCCTGGAG	CTCCAGGAAC	CAGGCAGTGA	3500
GGCCTTGGTC	TGAGACAGTA	TCCTCAGGTC	ACAGAGCAGA	GGATGCACAG	3550
GGTGTGCCAG	CAGTGAATGT	TTGCCCTGAA	TGCACACCAA	GGGCCCCACC	3600
TGCCACAGGA	CACATAGGAC	TCCACAGAGT	CTGGCCTCAC	CTCCCTACTG	3650
TCAGTCTGT	AGAATCGACC	TCTGCTGGCC	GGCTGTACCC	TGAGTACCCT	3700
CTCACTTCCT	CCTTCAGGTT	TTCAGGGGAC	AGGCCAACCC	AGAGGACAGG	3750
ATTCCCTGGA	GGCCACAGAG	GAGCACCAAG	GAGAAGATCT	GTAAGTAGGC	3800
CTTTGTTAGA	GTCTCCAAGG	TTCAGTTCTC	AGCTGAGGCC	TCTCACACAC	3850
TCCCTCTCTC	CCCAGGCCTG	TGGGTCTTCA	TTGCCCAGCT	CCTGCCACAC	3900
CTCCTGCCTG	CTGCCCTGAC	GAGAGTCATC			3930
ATG TCT CTT	GAG CAG AGG	AGT CTG CAC	TGC AAG CCT	GAG GAA	3972
GCC CTT GAG	GCC CAA CAA	GAG GCC CTG	GGC CTG GTG	TGT GTG	4014
CAG GCT GCC	ACC TCC TCC	TCT CCT CTG	GTC CTG GGC	ACC	4056
CTG GAG GAG	GTG CCC ACT	GCT GGG TCA	ACA GAT CCT	CCC CAG	4098
AGT CCT CAG	GGG GCC TCC	TTT CCC ACT	ACC ATC AAC	TTC	4140
ACT CGA CAG	AGG CAA CCC	AGT GAG GGT	TCC AGC AGC	CGT GAA	4182
GAG GAG GGG	CCA AGC ACC	TCT TGT ATC	CTG GAG TCC	TTG TTC	4224
CGA GCA GTA	ATC ACT AAG	AAG GTG GCT	GAT TTG GTT	GGT TTT	4266
CTG CTC CTC	AAA TAT CGA	GCC AGG GAG	CCA GTC ACA	AAG GCA	4308
GAA ATG CTG	GAG AGT GTC	ATC AAA AAT	TAC AAG CAC	TGT TTT	4350
CCT GAG ATC	TTC GGC AAA	GCC TCT GAG	TCC TTG CAG	CTG GTC	4392
TTT GGC ATT	GAC GTG AAG	GAA GCA GAC	CCC ACC GGC	CAC TCC	4434
TAT GTC CTT	GTC ACC TGC	CTA GGT CTC	TCC TAT GAT	GGC CTG	4476
CTG GGT GAT	AAT CAG ATC	ATG CCC AAG	ACA GGC TTC	CTG ATA	4518
ATT GTC CTG	GTC ATG ATT	GCA ATG GAG	GGC GGC CAT	GCT CCT	4560
GAG GAG GAA	ATC TGG GAG	GAG CTG AGT	GTG ATG GAG	GTG TAT	4602
GAT GGG AGG	GAG CAC AGT	GCC TAT GGG	GAG CCC AGG	AAG CTG	4644
CTC ACC CAA	GAT TTG GTG	CAG GAA AAG	TAC CTG GAG	TAC GGC	4686
AGG TGC CGG	ACA GTG ATC	CCG CAC GCT	ATG AGT TCC	TGT GGG	4728
GTC CAA GGG	CCC TCG CTG	AAA CCA GCT	ATG TGA		4761
AAGTCCTTGA	GTATGTGATC	AAGGTCAGTG	CAAGAGTTC		4800
GCTTTTTCTT	CCCATCCCTG	CGTGAAGCAG	CTTTGAGAGA	GGAGGAAGAG	4850
GGAGTCTGAG	CATGAGTTGC	AGCCAAGGCC	AGTGGGAGGG	GGACTGGGCC	4900
AGTGACACCT	CCAGGGCCGC	GTCCAGCAGC	TTCCCTGCCC	TCGTGTGACA	4950
TGAGGCCCAT	TCTTCACTCT	GAAGAGAGCG	GTCAGTGTTT	TCAGTAGTAG	5000
GTTTCTGTTC	TATTGGGTGA	CTTGGAGATT	TATCTTTGTT	CTCTTTTGGA	5050
ATTGTTCAAA	TGTTTTTTTT	TAAGGGATGG	TTGAATGAAC	TTCAGCATCC	5100
AAGTTTATGA	ATGACAGCAG	TCACACAGTT	CTGTGTATAT	AGTTTAAGGG	5150
TAAGAGTCTT	GTGTTTTTAT	CAGATTGGGA	AATCCATTCT	ATTTTGTGAA	5200
TTGGGATAAT	AACAGCAGTG	GAATAAGTAC	TTAGAAATGT	GAAAAATGAG	5250
CAGTAAATA	GATGAGATAA	AGAACTAAAG	AAATTAAGAG	ATAGTCAATT	5300
CTTGCCTTAT	ACCTCAGTCT	ATTCTGTAAA	ATTTTTAAAG	ATATATGCAT	5350
ACCTGGATT	CCTTGGCTTC	TTTGAGAAAT	TAAGAGAAAT	TAAATCTGAA	5400
TAAAGAATT	CTCCTGTTCA	CTGGCTCTTT	TCTTCTCCAT	GCACTGAGCA	5450
TCTGCTTTTT	GGAAGGCCCT	GGGTAGTAG	TGGAGATGCT	AAGGTAAGCC	5500
AGACTCATAC	CCACCCATAG	GGTCGTAGAG	TCTAGGAGCT	GCAGTCACGT	5550
AATCGAGGTG	GCAAGATGTC	CTCTAAAGAT	GTAGGGAAAA	GTGAGAGAGG	5600
GGTGAGGGTG	TGGGGCTCCG	GGTGAGAGTG	GTGGAGTGTG	AATGCCCTGA	5650
GCTGGGGCAT	TTTGGGCTTT	GGGAAACTGC	AGTTCCCTTCT	GGGGGAGCTG	5700
ATTGTAATGA	TCTTGGGTGG	ATCC			5724

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- (2) INFORMATION FOR SEQUENCE ID NO: 9:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4157 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-2 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCCATCCAGA	TCCCCATCCG	GGCAGAATCC	GGTTCCACCC	TTGCCGTGAA	50
CCCAGGGAAG	TCACGGGCCC	GGATGTGACG	CCACTGACTT	GCACATTGGA	100
GGTCAGAGGA	CAGCGAGATT	CTCGCCCTGA	GCAACGGCCT	GACGTCGGCG	150
GAGGGAAGCA	GGCGCAGGCT	CCGTGAGGAG	GCAAGGTAAG	ACGCCGAGGG	200
AGGACTGAGG	CGGGCCTCAC	CCCAGACAGA	GGGCCCCCAA	TTAATCCAGC	250
GCTGCCTCTG	CTGCCGGGCC	TGGACCACCC	TGCAGGGGAA	GACTTCTCAG	300
GCTCAGTCGG	CACCACCTCA	CCCCGCCACC	CCCCGCCGCT	TTAACC GCAG	350
GGAACCTCTGG	CGTAAGAGCT	TTGTGTGACC	AGGGCAGGGC	TGGTTAGAAG	400
TGCTCAGGGC	CCAGACTCAG	CCAGGAATCA	AGGTCAGGAC	CCCAAGAGGG	450
GACTGAGGGC	AACCCACCCC	CTACCCTCAC	TACCAATCCC	ATCCCCCAAC	500
ACCAACCCCA	CCCCCATCCC	TCAAACACCA	ACCCACCCCC	CAAACCCCAT	550
TCCCATCTCC	TCCCCACCA	CCATCCTGGC	AGAATCCGGC	TTTGCCCCCTG	600
CAATCAACCC	ACGGAAGCTC	CGGGAATGGC	GGCCAAGCAC	GCGGATCCTG	650
ACGTTACAT	GTACGGCTAA	GGGAGGGAAG	GGGTTGGGTC	TCGTGAGTAT	700
GGCCTTTGGG	ATGCAGAGGA	AGGGCCCAGG	CCTCCTGGAA	GACAGTGGAG	750
TCCTTAGGGG	ACCCAGCATG	CCAGGACAGG	GGGCCCCACTG	TACCCCTGTC	800
TCAAAC TGAG	CCACCTTTTC	ATTCAGCCGA	GGGAATCCTA	GGGATGCAGA	850
CCCACCTTCAG	GGGGTTGGGG	CCCAGCCTGC	GAGGAGTCAA	GGGGAGGAAG	900
AAGAGGGAGG	ACTGAGGGGA	CCTTGGAGTC	CAGATCAGTG	GCAACCTTGG	950
GCTGGGGGAT	CCTGGGCACA	GTGGCCGAAT	GTGCCCCGTG	CTCATTGCAC	1000
CTTCAGGGTG	ACAGAGAGTT	GAGGGCTGTG	GTCTGAGGGC	TGGGACTTCA	1050
GGTCAGCAGA	GGGAGGAATC	CCAGGATCTG	CCGGACCCAA	GGTGTGCCCC	1100
CTTCATGAGG	ACTCCCCATA	CCCCCGGCC	AGAAAGAAGG	GATGCCACAG	1150
AGTCTGGAAG	TAAATTGTTT	TTAGCTCTGG	GGGAACCTGA	TCAGGGATGG	1200
CCCTAAGTGA	CAATCTCATT	TGTACCACAG	GCAGGAGGTT	GGGGAACCCCT	1250
CAGGGAGATA	AGGTGTTGGT	GTAAAGAGGA	GCTGTCTGCT	CATTT CAGGG	1300
GGTTCCCCCT	TGAGAAAGGG	CAGTCCCTGG	CAGGAGTAAA	GATGAGTAAC	1350
CCACAGGAGG	CCATCATAAC	GTTCAACCCTA	GAACCAAAGG	GGTCAGCCCT	1400
GGACAACGCA	CGTGGGGTAA	CAGGATGTGG	CCCCTCCTCA	CTTGTCTTTC	1450
CAGATCTCAG	GGAGTTGATG	ACCTTGTTTT	CAGAAGGTGA	CTCAGTCAAC	1500
ACAGGGGCCC	CTCTGGTCTGA	CAGATGCAGT	GGTTCTAGGA	TCTGCCAAGC	1550
ATCCAGGTGG	AGAGCCTGAG	GTAGGATTGA	GGGTACCCCT	GGGCCAGAAT	1600
GCAGCAAGGG	GGCCCCATAG	AAATCTGCCC	TGCCCCCTGCG	GTTACTTCAG	1650
AGACCCTGGG	CAGGGCTGTC	AGCTGAAGTC	CCTCCATTAT	CTGGGATCCT	1700
TGATGTCTAG	GGAAGGGGAGG	CCTTGGTCTG	AAGGGGCTGG	AGTCAGGTCA	1750
GTAGAGGGAG	GGTCTCAGGC	CCTGCCAGGA	GTGGACGTGA	GGACCAAGCG	1800
GACTCGTCAC	CCAGGACACC	TGGACTCCAA	TGAATTTGAC	ATCTCTCGTT	1850
GTCCTTCGCG	GAGGACCTGG	TCACGTATGG	CCAGATGTGG	GTCCCCCTCTA	1900
TCTCCTTCTG	TACCATATCA	GGGATGTGAG	TTCTTGACAT	GAGAGATTCT	1950
CAAGCCAGCA	AAAGGGTG GG	ATTAGGCCCT	ACAAGGAGAA	AGGTGAGGGG	2000
CCTGAGTGAG	CACAGAGGGG	ACCCTCCACC	CAAGTAGAGT	GGGGACCTCA	2050
CGGAGTCTGG	CCAACCTTGC	TGAGACTTCT	GGGAATCCGT	GGCTGTGCTT	2100
GCAGTCTGCA	CACTGAAGGC	CCGTGCATTC	CTCTCCAGG	AATCAGGAGC	2150
TCCAGGAACG	AGGCAGTGAG	GCCTTGGTCT	GAGTCAGTGC	CTCAGGTCA	2200
AGAGCAGAGG	GGAGCGAGAG	AGTGCCAACA	CTGAAGGTTT	GCCTGGAATG	2250
CACACCAAGG	GGCCACCCCG	CCCAGAACAA	ATGGGACTCC	AGAGGGCCTG	2300
GCCTCACCCCT	CCCTATTCTC	AGTCCTGCAG	CCTGAGCATG	TGCTGGCCGG	2350
CTGTACCCTG	AGGTGCCCTC	CCACTTCCTC	CTTCAGGTTT	TGAGGGGGAC	2400
AGGCTGACAA	GTAGGACCCG	AGGCACTGGA	GGAGCATTGA	AGGAGAAGAT	2450
CTGTAAAGTAA	GCCCTTGTC	GAGCCTCCAA	GGTTCAGTTT	AGTTCTCACC	2500
TAAGGCCTCA	CACACGCTCC	TTCTCTCCCC	AGGCCTGTGG	GTCTTCATTG	2550
CCCAGCTCCT	GGCCGCACTC	CTGCCTGCTG	CCCTGACCAG	AGTCATC	2597
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	2639
GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG GTG	GGT GCG	2681
CAG GCT CCT	GCT ACT GAG	GAG CAG CAG	ACC GCT TCT	TCC TCT	2723

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TCT ACT CTA GTG GAA GTT ACC CTG GGG GAG GTG CCT GCT GCC	2765
GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC	2807
TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT	2849
GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATG TTT	2891
CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC AGT AGG AAG	2933
ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC	2975
AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGT GTC CTC	3017
AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC	3059
TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTG GAA	3101
GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG	3143
GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG	3185
CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA	3227
ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG	3269
CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG GAC AGT GTC	3311
TTC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG	3353
GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT	3395
GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA	3437
ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT	3479
GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT	3521
TTG AGA GAG GGA GAA GAG TGA	3542
GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT	3592
GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA	3642
GGCCCATTC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG	3692
TTTCTGTTCT GTTGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA	3742
TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA	3792
GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG	3842
TAAGAGTCCT GTTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG	3892
TTGTACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG	3942
AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT	3992
TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT	4042
TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT	4092
TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC	4142
CCTGGTAGTA GTGGG	4157

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- (2) INFORMATION FOR SEQUENCE ID NO: 10:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 662 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-21 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATCCCCAT	GGATCCAGGA	AGAATCCAGT	TCCACCCCTG	CTGTGAACCC	50
AGGGAAGTCA	CGGGGCCGGA	TGTGACGCCA	CTGACTTGCG	CGTTGGAGGT	100
CAGAGAAACAG	CGAGATTCTC	GCCCTGAGCA	ACGGCCTGAC	GTCGGCGGAG	150
GGAAGCAGGC	GCAGGCTCCG	TGAGGAGGCA	AGGTAAGATG	CCGAGGGAGG	200
ACTGAGGCGG	GCCTCACCCC	AGACAGAGGG	CCCCCAATAA	TCCAGCGCTG	250
CCTCTGCTGC	CAGGCCTGGA	CCACCCTGCA	GGGGAAGACT	TCTCAGGCTC	300
AGTCGCCACC	ACCTCACCCC	GCCACCCCCC	GCCGCTTTAA	CCGCAGGGAA	350
CTCTGGTGTA	AGAGCTTTGT	GTGACCAGGG	CAGGGCTGGT	TAGAAGTGCT	400
CAGGGCCCAG	ACTCAGCCAG	GAATCAAGGT	CAGGACCCCA	AGAGGGGACT	450
GAGGGTAACC	CCCCCGCACC	CCCACCACCA	TTCCCATCCC	CCAACACCAA	500
CCCCACCCCC	ATCCCCCAAC	ACCAAACCCA	CCACCATCGC	TCAAACATCA	550
ACGGCACCCC	CAAACCCCGA	TTCCCATCCC	CACCCATCCT	GGCAGAATCG	600
GAGCTTTGCC	CCTGCAATCA	ACCCACGGAA	GCTCCGGGAA	TGGCGGCCAA	650
GCACGCGGAT	CC				662

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- (2) INFORMATION FOR SEQUENCE ID NO: 11:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1640 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA to mRNA
 (ix) FEATURE:
 (A) NAME/KEY: cDNA MAGE-3
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCCGCGAGGG AAGCCGGCCC AGGCTCGGTG AGGAGGCAAG GTTCTGAGGG 50
 GACAGGCTGA CCTGGAGGAC CAGAGGCCCC CGGAGGAGCA CTGAAGGAGA 100
 AGATCTGCCA GTGGGTCTCC ATTGCCCAGC TCCTGCCAC ACTCCCGCCT 150
 GTTGCCCTGA CCAGAGTCAT C 171
 ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA 213
 GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG 255
 CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT 297
 TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC 339
 GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC 381
 CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT 423
 GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC 465
 CCT GAC CTG GAG TCC GAG TTC CAA GCA GCA CTC AGT AGG AAG 507
 GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 549
 AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC 591
 GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT 633
 TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA 675
 GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG 717
 GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG 759
 CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA 801
 AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG 843
 CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG 885
 TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG 927
 GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT 969
 GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA 1011
 ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT 1053
 GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT 1095
 TTG AGA GAG GGG GAA GAG TGA 1116
 GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT 1166
 GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCTCC TGTGACGTGA 1216
 GGCCCATCT TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG 1266
 TTTCTGTTCT GTTGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG 1316
 TTGTTCAAAT GTTCCTTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG 1366
 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG 1416
 TAAGAGTCTT GttTTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA 1466
 TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC 1516
 GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG 1566
 ATTCTTGCTT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA 1616
 ACCAGGATTT CCTTGACTTC TTG 1640

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- (2) INFORMATION FOR SEQUENCE ID NO: 12:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 943 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-31 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGATCCTCCA	CCCCAGTAGA	GTGGGGACCT	CACAGAGTCT	GGCCAACCT	50
CCTGACAGTT	CTGGGAATCC	GTGGCTGCGT	TTGCTGTCTG	CACATTGGGG	100
GCCCGTGGAT	TCCTCTCCCA	GGAATCAGGA	GCTCCAGGAA	CAAGGCAGTG	150
AGGACTTGGT	CTGAGGCAGT	GTCCTCAGGT	CACAGAGTAG	AGGGGgCTCA	200
GATAGTGCCA	ACGGTGAAGG	TTTGCCTTGG	ATTCAAACCA	AGGGCCCCAC	250
CTGCCCCAGA	ACACATGGAC	TCCAGAGCGC	CTGGCCTCAC	CCTCAATACT	300
TTCACTCCTG	CAGCCTCAGC	ATGCGCTGGC	CGGATGTACC	CTGAGGTGCC	350
CTCTCACTTC	CTCCTTCAGG	TTCTGAGGGG	ACAGGCTGAC	CTGGAGGACC	400
AGAGGCCCCC	GGAGGAGCAC	TGAAGGAGAA	GATCTGTAAG	TAAGCCTTTG	450
TTAGAGCCTC	CAAGGTTCCA	TTCAGTACTC	AGCTGAGGTC	TCTCACATGC	500
TCCCTCTCTC	CCCAGGCCAG	TGGGTCTCCA	TTGCCCAGCT	CCTGCCCCACA	550
CTCCCGCCTG	TTGCCCTGAC	CAGAGTCATC			580
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	622
GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG GTG	GGT GCG	664
CAG GCT CCT	GCT ACT GAG	GAG CAG GAG	GCT GCC TCC	TCC TCT	706
TCT AGT GTA	GTT GAA GTC	ACC CTG GGG	GAG GTG CCT	GCT GCC	748
GAG TCA CCA	GAT CCT CCC	CAG AGT CCT	CAG GGA GCC	TCC AGC	790
CTC CCC ACT	ACC ATG AAC	TAC CCT CTC	TGG AGC CAA	TCC TAT	832
GAG GAC TCC	AGC AAC CAA	GAA GAG GAG	GGG CCA AGC	ACC TTC	874
CCT GAC CTG	GAG TCT GAG	TTC CAA GCA	GCA CTC AGT	AGG AAG	916
GTG GCC AAG	TTG GTT CAT	TTT CTG CTC			943

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- (2) INFORMATION FOR SEQUENCE ID NO: 13:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2531 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-4 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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GGATCCAGGC	CCTGCCTGGA	GAAATGTGAG	GGCCCTGAGT	GAACACAGTG	50
GGGATCATCC	ACTCCATGAG	AGTGGGGACC	TCACAGAGTC	CAGCCTACCC	100
TCTTGATGGC	ACTGAGGGAC	CGGGGCTGTG	CTTACAGTCT	GCACCCTAAG	150
GGCCCATGGA	TTCTCTCCT	AGGAGCTCCA	GGAACAAGGC	AGTGAGGCCT	200
TGGTCTGAGA	CAGTGTCCCT	AGGTTACAGA	GCAGAGGATG	CACAGGCTGT	250
GCCAGCAGTG	AATGTTTGCC	CTGAATGCAC	ACCAAGGGCC	CCACCTGCCA	300
CAAGACACAT	AGGACTCCAA	AGAGTCTGGC	CTCACCTCCC	TACCATCAAT	350
CCTGCAGAAT	CGACCTCTGC	TGGCCGGCTA	TACCCTGAGG	TGCTCTCTCA	400
CTTCCTCCTT	CAGGTTCTGA	GCAGACAGGC	CAACCGGAGA	CAGGATTCCC	450
TGGAGGCCAC	AGAGGAGCAC	CAAGGAGAAG	ATCTGTAAGT	AAGCCTTTGT	500
TAGAGCCTCT	AAGATTGGT	TCTCAGCTGA	GGTCTCTCAC	ATGCTCCCTC	550
TCTCCGTAGG	CCTGTGGGTC	CCCATTGCCC	AGCTTTTGCC	TGCACTCTTG	600
CCTGCTGCCC	TGACCAGAGT	CATC			624
ATG TCT TCT	GAG CAG AAG AGT	CAG CAC TGC AAG	CCT GAG GAA		666
GGC GTT GAG	GCC CAA GAA GAG	GCC CTG GGC CTG	GTG GGT GCA		708
CAG GCT CCT	ACT ACT GAG GAG	CAG GAG GCT GCT	GTC TCC TCC		750
TCC TCT CCT	CTG GTC CCT GGC	ACC CTG GAG GAA	GTG CCT GCT		792
GCT GAG TCA	GCA GGT CCT CCC	CAG AGT CCT CAG	GGA GCC TCT		834
GCC TTA CCC	ACT ACC ATC AGC	TTC ACT TGC TGG	AGG CAA CCC		876
AAT GAG GGT	TCC AGC AGC CAA	GAA GAG GAG GGG	CCA AGC ACC		918
TCG CCT GAC	GCA GAG TCC TTG	TTC CGA GAA GCA	CTC AGT AAC		960
AAG GTG GAT	GAG TTG GCT CAT	TTT CTG CTC CGC	AAG TAT CGA		1002
GCC AAG GAG	CTG GTC ACA AAG	GCA GAA ATG CTG	GAG AGA GTC		1044
ATC AAA AAT	TAC AAG CGC TGC	TTT CCT GTG ATC	TTC GGC AAA		1086
GCC TCC GAG	TCC CTG AAG ATG	ATC TTT GGC ATT	GAC GTG AAG		1128
GAA GTG GAC	CCC GCC AAG AAC	ACC TAC ACC CTT	GTC ACC TGC		1170
CTG GGC CTT	TCC TAT GAT GGC	CTG CTG GGT AAT	AAT CAG ATC		1212
TTT CCC AAG	ACA GGC CTT CTG	ATA ATC GTC CTG	GGC ACA ATT		1254
GCA ATG GAG	GGC GAC AGC GCC	TCT GAG GAG GAA	ATC TGG GAG		1296
GAG CTG GGT	GTG ATG GGG GTG	TAT GAT GGG AGG	GAG CAC ACT		1338
GTC TAT GGG	GAG CCC AGG AAA	CTG CTC ACC CAA	GAT TGG GTG		1380
CAG GAA AAC	TAC CTG GAG TAC	CGG CAG GTA CCC	GGC AGT AAT		1422
CCT GCG CGC	TAT GAG TTC CTG	TGG GGT CCA AGG	GCT CTG GCT		1464
GAA ACC AGC	TAT GTG AAA GTC	CTG GAG CAT GTG	GTC AGG GTC		1506
AAT GCA AGA	GTT CGC ATT GCC	TAC CCA TCC CTG	CGT GAA GCA		1548
GCT TTG TTA	GAG GAG GAA GAG	GGA GTC TGA			1578
GCATGAGTTG	CAGCCAGGGC	TGTGGGGAAG	GGGCAGGGCT	GGGCCAGTGC	1628
ATCTAACAGC	CCTGTGCAGC	AGCTTCCCTT	GCCTCGTGTA	ACATGAGGCC	1678
CATTCTTCAC	TCTGTTTGAA	GAAAATAGTC	AGTGTTCCTTA	GTAGTGGGTT	1728
TCTATTTTGT	TGGATGACTT	GGAGATTTAT	CTCTGTTTCC	TTTTACAATT	1778
GTTGAAATGT	TCCTTTTAAT	GGATGGTTGA	ATTAACCTCA	GCATCCAAGT	1828
TTATGAATCG	TAGTTAACGT	ATATTGCTGT	TAATATAGTT	TAGGAGTAAG	1878
AGTCTTGTTT	TTTATTCAGA	TTGGGAAATC	CGTTCATTTT	TGTGAATTTG	1928
GGACATAATA	ACAGCAGTGG	AGTAAGTATT	TAGAAGTGTG	AATTCACCGT	1978
GAAATAGGTG	AGATAAATTA	AAAGATACTT	AATTCCTGCC	TTATGCCTCA	2028
GTCTATTCTG	TAAAATTTAA	AAATATATAT	GCATACCTGG	ATTTCTCTGG	2078
CTTCGTGAAT	GTAAGAGAAA	TTAAATCTGA	ATAAATAATT	CTTTCTGTTA	2128
ACTGGCTCAT	TTCTTCTCTA	TGCACTGAGC	ATCTGCTCTG	TGGAAGGCCC	2178
AGGATTAGTA	GTGGAGATAC	TAGGGTAAGC	CAGACACACA	CCTACCGATA	2228
GGGTATTAAG	AGTCTAGGAG	CGCGGTCATA	TAATTAAGGT	GACAAGATGT	2278
CCTCTAAGAT	GTAGGGGAAA	AGTAACGAGT	GTGGGTATGG	GGCTCCAGGT	2328
GAGAGTGGTC	GGGTGTAAAT	TCCCTGTGTG	GGGCCTTTTG	GGCTTTGGGA	2378
AACTGCATTT	TCTTCTGAGG	GATCTGATTG	TAATGAAGCT	TGGTGGGTCC	2428
AGGGCCAGAT	TCTCAGAGGG	AGAGGGAAAA	GCCCAGATTG	GAAAAGTTGC	2478

TCTGAGCAGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT
GGG

2528
2531

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- (2) INFORMATION FOR SEQUENCE ID NO: 14:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2531 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-41 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG 50
 GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC 100
 TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG 150
 GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT 200
 TGGTCTGAGA CAGTGTCTCT AGGTTACAGA GCAGAGGATG CACAGGCTGT 250
 GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA 300
 CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT 350
 CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA 400
 CTTCTCTCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC 450
 TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT 500
 TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC 550
 TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACCTTG 600
 CCTGCTGCCC TGAGCAGAGT CATC 624
 ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 666
 GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCG 708
 CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC 750
 TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT 792
 GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT 834
 GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC 876
 AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC 918
 TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC 960
 AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA 1002
 GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC 1044
 ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA 1086
 GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG 1128
 GAA GTG GAC CCC ACC AGC AAC ACC TAC ACC CTT GTC ACC TGC 1170
 CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC 1212
 TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT 1254
 GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG 1296
 GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT 1338
 GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG 1380
 CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT 1422
 CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT 1464
 GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC 1506
 AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA 1548
 GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA 1578
 GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC 1628
 ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC 1678
 CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTCTTCA GTAGTGGGTT 1728
 TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT 1778
 GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACCTCA GCATCCAAGT 1828
 TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG 1878
 AGTCTTGTTT TTTATTGAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG 1928
 GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTACCCGT 1978
 GAAATAGGTG AGATAAATTA AAAGATACTT AATTCGCCCTTATGCCTCA 2028
 GTCTATTCTG TAAATTTTAA AAATATATAT GCATACCTGG ATTTCTCTGG 2078
 CTTCTGTAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTGA 2128
 ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC 2178
 AGGATTAGTA TGGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA 2228
 GGGTATTAAG AGCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT 2278
 CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT 2328
 GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA 2378
 AACTCCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC 2428

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AGGGCCAGAT	TCTCAGAGGG	AGAGGGAAAA	GCCCAGATTG	GAAAAGTTGC	2478
TCTGAGCGGT	TCCTTTGTGA	CAATGGATGA	ACAGAGAGGA	GCCTCTACCT	2528
GGG					2531

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- (2) INFORMATION FOR SEQUENCE ID NO: 15:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1068 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA to mRNA
 (ix) FEATURE:
 (A) NAME/KEY: cDNA MAGE-4
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

G GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA	40
GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG	82
CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA	124
ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT	166
GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT	208
GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC	250
ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG	292
GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC	334
GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG	376
GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT	418
GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC	460
ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG	502
GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT	544
CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG	586
CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA	628
TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC	670
TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG	720
TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG	770
GCCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTT TTAGTAGTGG	820
GTTTCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA	870
ATTGTTGAAA TGTTCTTTT AATGGATGGT TGAATTA ACT TCAGCATCCA	920
AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT	970
AAGAGTCTTG TTTTTTATTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT	1020
TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC	1068

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- (2) INFORMATION FOR SEQUENCE ID NO: 16:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2226 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-5 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG 50
 GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC 100
 TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCTGAG 150
 GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCCT 200
 TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC 250
 TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC 300
 GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG 350
 TCAGTCTGTC AGAATCAGCC TCTGCTTGCT TGTGTACCTT GAGGTGCCCT 400
 CTCACCTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG 450
 GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG 500
 ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTTCA TTTTAGCTGA 550
 GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC 600
 AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC 644
 ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 684
 CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG 728
 GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA 770
 TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA 812
 AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC 854
 CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG 896
 TGG CTG ACT TGA 908
 TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCTGGT CACAAAGGCA 958
 GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT 1008
 CTTGCGCAAA GCCTCCGAGT CTTGTCAGCT GGTCTTTGGC ATTGACGTGA 1058
 AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA 1108
 CTCCTATGAT GGCCTGCTGG TTGATAATAA TCAGATCATG CCCAAGACGG 1158
 GCCTCCTGAT AATCGTCTTG GGCATGATTG CAATGGAGGG CAAATGCGTC 1208
 CCTGAGGAGA AAATCTGGGA GGAGCTGAGT GTGATGAAGG TGTATGTTGG 1258
 GAGGGAGCAC AGTGTCTGTG GGGAGCCCAG GAAGCTGCTC ACCCAAGATT 1308
 TGGTGCAGGA AAATACCTG GAGTACCGGC AGGTGCCCCAG CAGTGATCCC 1358
 ATATGCTATG AGTTACTGTG GGGTCCAAGG GCACTCGCTG CTTGAAAGTA 1408
 CTGGAGCACG TGGTCAGGGT CAATGCAAGA GTTCTCATTT CCTACCCATC 1458
 CCTGCGTGAA GCAGCTTTGA GAGAGGAGGA AGAGGGAGTC TGAGCATGAG 1508
 CTGCAGCCAG GGCCACTGCG AGGGGGGCTG GGCCAGTGCA CCTTCCAGGG 1558
 CTCCTGCCAG TAGTTTCCCC TGCCTTAATG TGACATGAGG CCCATTCTTC 1608
 TCTCTTTGAA GAGAGCAGT AACATTCTTA GTAGTGGGTT TCTGTTCTAT 1658
 TGGATGACTT TGAGATTTGT CTTTGTTCCT TTTTGGGAAT GTTCAAATGT 1708
 TTCTTTTAAAT GGGTGGTTGA ATGAACCTCA GCATTCAAAT TTATGAATGA 1758
 CAGTAGTCAC ACATAGTGCT GTTTATATAG TTTAGGAGTA AGAGTCTTGT 1808
 TTTTATTCA GATTGGGAAA TCCATTCCAT TTTGTGAAT GGGACATAGT 1858
 TACAGCAGTG GAATAAGTAT TCATTTAGAA ATGTGAATGA GCAGTAAAC 1908
 TGATGACATA AAGAAATTAA AAGATATTTA ATTCTTGCTT ATACTCAGTC 1958
 TATTCGGTAA AATTTTTTTT AAAAAATGTG CATACCTGGA TTTCCCTTGGC 2008
 TTCTTTGAGA ATGTAAGACA AATTAAATCT GAATAAATCA TTCTCCCTGT 2058
 TCACTGGCTC ATTTATTCTC TATGCACTGA GCATTGTGCTC TGTGGAAGGC 2108
 CCTGGGTTAA TAGTGGAGAT GCTAAGGTAA GCCAGACTCA CCCCTACCCA 2158
 CAGGGTAGTA AAGTCTAGGA GCAGCAGTCA TATAATTAAG GTGGAGAGAT 2208
 GCCCTCTAAG ATGTAGAG 2226

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- (2) INFORMATION FOR SEQUENCE ID NO: 17:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2305 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-51 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG 50
 GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC 100
 TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG 150
 GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT 200
 TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC 250
 TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC 300
 GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG 350
 TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCCT GAGGTGCCCT 400
 CTCACCTTTT CTTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG 450
 GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG 500
 ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCACT TTTTAGCTGA 550
 GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC 600
 AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC 644
 ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 686
 GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG TGG GTG TGC 728
 AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT CCT CCT CCT 770
 CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG 812
 GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA 854
 TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA 896
 AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC 938
 CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG 980
 TGG CTG ACT TGA 992
 TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCCGGT CACAAAGGCA 1042
 GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT 1092
 CTTCCGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA 1142
 AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA 1192
 CTCCTATGAT GGCCTGGTGG TTTAATCAGA TCATGCCCAA GACGGGCCTC 1242
 CTGATAATCG TCTTGGGCAT GATTGCAATG GAGGGCAAAT GCGTCCCTGA 1292
 GGAGAAAATC TGGGAGGAGC TGGGTGTGAT GAAGGTGTAT GTTGGGAGGG 1342
 AGCACAGTGT CTGTGGGGAG CCCAGGAAGC TGCTCACCCA AGATTTGGTG 1392
 CAGGAAAAC TACCTGGAGTA CCGCAGGTGC CCAGCAGTGA TCCCATATGC 1442
 TATGAGTTAC TGTGGGGTCC AAGGGCACTC GCTGCTTGAA AGTACTGGAG 1492
 CACGTGGTCA GGGTCAATGC AAGAGTTCTC ATTTCCCTACC CATCCCTGCA 1542
 TGAAGCAGCT TTGAGAGAGG AGGAAGAGGG AGTCTGAGCA TGAGCTGCAG 1592
 CCAGGGCCAC TGCAGAGGGG GCTGGGCCAG TGCACCTTCC AGGGCTCCGT 1642
 CCAGTAGTTT CCCCTGCCTT AATGTGACAT GAGGCCATT CTTCTCTCTT 1692
 TGAAGAGAGC AGTCAACATT CTTAGTAGTG GGTCTTCTGT CTATTGGATG 1742
 ACTTTGAGAT TTGTCTTTGT TTCCTTTTGG AATTGTTCAA ATGTTCCCTT 1792
 TAATGGGTGG TTGAATGAAC TTCAGCATT CAAATTTATGA ATGACAGTAG 1842
 TCACACATAG TGCTGTTTAT ATAGTTTAGG AGTAAGAGTC TTGTTTTTTA 1892
 TTCAGATTGG GAAATCCATT CCATTTTGTG AATTGGGACA TAGTTACAGC 1942
 AGTGGAATAA GTATTCATTT AGAAATGTGA ATGAGCAGTA AACTGATGA 1992
 GATAAAGAAA TTAAAAGATA TTTAATTCTT GCCTTATACT CAGTCTATTC 2042
 GGTAATAATTT TTTTTTAAAA ATGTGCATAC CTGGATTTCC TTGGCTTCTT 2092
 TGAGAATGTA AGACAAATTA AATCTGAATA AATCATTCTC CCTGTTCACT 2142
 GGCTCATTTA TTCTCTATGC ACTGAGCATT TGCTCTGTGG AAGGCCCTGG 2192
 GTTAATAGTG GAGATGCTAA GGTAAGCCAG ACTCACCCCT ACCCACAGGG 2242
 TAGTAAAGTC TAGGAGCAGC AGTCATATAA TTAAGGTGGA GAGATGCCCT 2292
 CTAAGATGTA GAG 2305

009250.4567560

- (2) INFORMATION FOR SEQUENCE ID NO: 18:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-6 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TAT	TTC	TTT	CCT	GTG	ATC	TTC	AGC	AAA	GCT	TCC	GAT	TCC	TTG	42
CAG	CTG	GTC	TTT	GGC	ATC	GAG	CTG	ATG	GAA	GTG	GAC	CCC	ATC	84
GGC	CAC	GTG	TAC	ATC	TTT	GCC	ACC	TGC	CTG	GGC	CTC	TCC	TAC	126
GAT	GGC	CTG	CTG	GGT	GAC	AAT	CAG	ATC	ATG	CCC	AGG	ACA	GGC	168
TTC	CTG	ATA	ATC	ATC	CTG	GCC	ATA	ATC	GCA	AGA	GAG	GGC	GAC	210
TGT	GCC	CCT	GAG	GAG										225

009250" 54562560

- (2) INFORMATION FOR SEQUENCE ID NO: 19:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1947 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-7 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

005250" 057543" 052600

TGAATGGACA	ACAAGGGCCC	CACACTCCCC	AGAACACAAG	GGACTCCAGA	50
GAGCCCAGCC	TCACCTTCCC	TACTGTCACT	CCTGCAGCCT	CAGCCTCTGC	100
TGGCCGGCTG	TACCCTGAGG	TGCCCTCTCA	CTTCCTCCTT	CAGGTTCTCA	150
GCGGACAGGC	CGGCCAGGAG	GTCAGAAGCC	CCAGGAGGCC	CCAGAGGAGC	200
ACCGAAGGAG	AAGATCTGTA	AGTAGGCCTT	TGTTAGGGCC	TCCAGGGCGT	250
GGTTTCACAA	TGAGGCCCCC	CACAAGCTCC	TTCTCTCCCC	AGATCTGTGG	300
GTTCCCTCCC	ATCGCCCAGC	TGCTGCCCGC	ACTCCAGCCT	GCTGCCCTGA	350
CCAGAGTCAT	CATGTCTTCT	GAGCAGAGGA	GTCAGCACTG	CAAGCCTGAG	400
GATGCCTTGA	GGCCCCAAGGA	CAGGAGGCTC	TGGGCCTGGT	GGGTGCGCAG	450
GCTCCCGCCA	CCGAGGAGCA	CGAGGCTGCC	TCCTCCTTCA	CTCTGATTGA	500
AGGCACCCCT	GAGGAGGTGC	CTGCTGCTGG	GTCCCCCAGT	CCTCCCCTGA	550
GTCTCAGGGT	TCCTCCTTTT	CCCTGACCAT	CAGCAACAAC	ACTCTATGGA	600
GCCAATCCAG	TGAGGGCACC	AGCAGCCGGG	AAGAGGAGGG	GCCAACCACC	650
TAGACACACC	CCGCTCACCT	GGCGTCCTTG	TTCCA		685
ATG GGA AGG	TGG CTG AGT	TGG TTC GCT	TCC TGC TGC	ACA AGT	727
ATC GAG TCA	AGG AGC TGG	TCA CAA AGG	CAG AAA TGC	TGG ACA	769
GTG TCA TCA	AAA ATT ACA	AGC ACT AGT	TTC CTT GTG	ATC TAT	811
GGC AAA GCC	TCA GAG TGC	ATG CAG GTG	ATG TTT GGC	ATT GAC	853
ATG AAG GAA	GTG GAC CCC	GCG GCC ACT	CCT ACG TCC	TTG TCA	895
CCT GCT TGG	GCC TCT CCT	ACA ATG GCC	TGC TGG GTG	ATG ATC	937
AGA GCA TGC	CCG AGA CCG	GCC TTC TGA			964
TTATGGTCTT	GACCATGATC	TTAATGGAGG	GCCACTGTGC	CCCTGAGGAG	1014
GCAATCTGGG	AAGCGTTGAG	TGTAATGGTG	TATGATGGGA	TGGAGCAGTT	1064
TCTTTGGGCA	GCTGAGGAAG	CTGCTCACCC	AAGATTGGGT	GCAGGAAAAC	1114
TACCTGCAAT	ACCGCCAGGT	GCCCAGCAGT	GATCCCCCGT	GCTACCACTT	1164
CCTGTGGGGT	CCAAGGGCCC	TCATTGAAAC	CAGCTATGTG	AAAGTCCTGG	1214
AGTATGCAGC	CAGGGTCAGT	ACTAAAGAGA	GCATTTCTTA	CCCATCCCTG	1264
CATGAAGAGG	CTTTGGGAGA	GGAGGAAGAG	GGAGTCTGAG	CAGAAGTTGC	1314
AGCCAGGGCC	AGTGGGGCAG	ATTGGGGGAG	GGCCTGGGCA	GTGCACGTTT	1364
CACACATCCA	CCACCTTCCC	TGTCCTGTTA	CATGAGGCC	ATTCTTCACT	1414
CTGTGTTTGA	AGAGAGCAGT	CAATGTTCTC	AGTAGCGGGG	AGTGTGTTGG	1464
GTGTGAGGGA	ATACAAGGTG	GACCATCTCT	CAGTTCCTGT	TCTCTTGGGC	1514
GATTTGGAGG	TTTATCTTTG	TTTCCTTTTG	CAGTCGTTCA	AATGTTCTTT	1564
TTAATGGATG	GTGTAATGAA	CTTCAACATT	CATTTTCATG	ATGACAGTAG	1614
GCAGACTTAC	TGTTTTTTAT	ATAGTTAAAA	GTAAGTGCAT	TGTTTTTTAT	1664
TTATGTAAGA	AAATCTATGT	TATTTCTTGA	ATTGGGACAA	CATAACATAG	1714
CAGAGGATTA	AGTACCTTTT	ATAATGTGAA	AGAACAAAGC	GGTAAAATGG	1764
GTGAGATAAA	GAAATAAAGA	AATTAAATTG	GCTGGGCACG	GTGGCTCACG	1814
CCTGTAATCC	CAGCACTTTA	GGAGGCAGAG	GCACGGGGAT	CACGAGGTCA	1864
GGAGATCGAG	ACCATTCTGG	CTAACACAGT	GAAACACCAT	CTCTATTAAA	1914
AATACAAAAC	TTAGCCGGGC	GTGGTGCGCG	GTG		1947

- (2) INFORMATION FOR SEQUENCE ID NO: 20:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1810 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-8 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GAGCTCCAGG AACAGGCTG TGAGGTCTTG GTCTGAGGCA GTATCTTCAA 50
 TCACAGAGCA TAAGAGGCC AGGCAGTAGT AGCAGTCAAG CTGAGGTGGT 100
 GTTTCCCTTG TATGTATACC AGAGGCCCTT CTGGCATCAG AACAGCAGGA 150
 ACCCCACAGT TCCTGGCCCT ACCAGCCCTT TTGTCTAGTCC TGGAGCCTTG 200
 GCCTTTGCCA GGAGGCTGCA CCCTGAGATG CCCTCTCAAT TTCTCCTTCA 250
 GGTTCCGAGA GAACAGGCCA GCCAGGAGGT CAGGAGGCCC CAGAGAAGCA 300
 CTGAAGAAGA CCTGTAAGTA GACCTTTGTT AGGGCATCCA GGGTGTAGTA 350
 CCCAGCTGAG GCCTCTCACA CGCTTCCTCT CTCCCCAGGC CTGTGGGTCT 400
 CAATTGCCCA GCTCCGGCCC AACTCTCCT GCTGCCCTGA CCTGAGTCAT 450
 C 451
 ATG CTT CTT GGG CAG AAG AGT CAG CGC TAC AAG GCT GAG GAA 493
 GGC CTT CAG GCC CAA GGA GAG GCA CCA GGG CTT ATG GAT GTG 535
 CAG ATT CCC ACA GCT GAG GAG CAG AAG GCT GCA TCC TCC TCC 577
 TCT ACT CTG ATC ATG GGA ACC CTT GAG GAG GTG ACT GAT TCT 619
 GGG TCA CCA AGT CCT CCC CAG AGT CCT GAG GGT GCC TCC TCT 661
 TCC CTG ACT GTC ACC GAC AGC ACT CTG TGG AGC CAA TCC GAT 703
 GAG GGT TCC AGC AGC AAT GAA GAG GAG GGG CCA AGC ACC TCC 745
 CCG GAC CCA GCT CAC CTG GAG TCC CTG TTC CGG GAA GCA CTT 787
 GAT GAG AAA GTG GCT GAG TTA GTT CGT TTC CTG CTC CGC AAA 829
 TAT CAA ATT AAG GAG CCG GTC ACA AAG GCA GAA ATG CTT GAG 871
 AGT GTC ATC AAA AAT TAC AAG AAC CAC TTT CCT GAT ATC TTC 913
 AGC AAA GCC TCT GAG TGC ATG CAG GTG ATC TTT GGC ATT GAT 955
 GTG AAG GAA GTG GAC CCT GCC GGC CAC TCC TAC ATC CTT GTC 997
 ACC TGC CTG GGC CTC TCC TAT GAT GGC CTG CTG GGT GAT GAT 1039
 CAG AGT ACG CCC AAG ACC GGC CTC CTG ATA ATC GTC CTG GGC 1081
 ATG ATC TTA ATG GAG GGC AGC CGC GCC CCG GAG GAG GCA ATC 1123
 TGG GAA GCA TTG AGT GTG ATG GGG GCT GTA TGA 1156
 TGGGAGGGAG CACAGTGTCT ATTGGAAGCT CAGGAAGCTG CTCACCCAAG 1206
 AGTGGGTGCA GGAGAACTAC CTGGAGTACC GCCAGGCGCC CGGCAGTGAT 1256
 CCTGTGCGCT ACGAGTTCCT GTGGGGTCCA AGGGCCCTTG CTGAAACCAG 1306
 CTATGTGAAA GTCCTGGAGC ATGTGGTCAG GGTCAATGCA AGAGTTCGCA 1356
 TTTCTTACCC ATCCCTGCAT GAAGAGGCTT TGGGAGAGGA GAAAGGAGTT 1406
 TGAGCAGGAG TTGCAGCTAG GGCCAGTGGG GCAGGTTGTG GGAGGGCCTG 1456
 GGCCAGTGCA CGTTCCAGGG CCACATCCAC CACTTCCCT GCTCTGTTAC 1506
 ATGAGGCCCA TTCTTCACTC TGTGTTTGAA GAGAGCAGTC ACAGTTCTCA 1556
 GTAGTGGGGA GCATGTTGGG TGTGAGGGAA CACAGTGTGG ACCATCTCTC 1606
 AGTTCCTGTT CTATTGGGCG ATTTGGAGGT TTATCTTTGT TTCCTTTTGG 1656
 AATTGTTCCA ATGTTCCCTT TAATGGATGG TGTAATGAAC TTCAACATTG 1706
 ATTTTATGTA TGACAGTAGA CAGACTTACT GCTTTTATA TAGTTTAGGA 1756
 GTAAGAGTCT TGCTTTTCAT TTATACTGGG AAACCCATGT TATTTCTTGA 1806
 ATTC 1810

009250*E4562560

- (2) INFORMATION FOR SEQUENCE ID NO: 21:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1412 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-9 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

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TCTGAGACAG	TGTCCTCAGG	TCGCAGAGCA	GAGGAGACCC	AGGCAGTGTC	50
AGCAGTGAAG	GTGAAGTGTT	CACCCTGAAT	GTGCACCAAG	GGCCCCACCT	100
GCCCCAGCAC	ACATGGGACC	CCATAGCACC	TGGCCCCATT	CCCCCTACTG	150
TCACTCATAG	AGCCTTGATC	TCTGCAGGCT	AGCTGCACGC	TGAGTAGCCC	200
TCTCACTTCC	TCCCTCAGGT	TCTCGGGACA	GGCTAACCAG	GAGGACAGGA	250
GCCCCAAGAG	GCCCCAGAGC	AGCACTGACG	AAGACCTGTA	AGTCAGCCTT	300
TGTTAGAACC	TCCAAGGTTT	GGTTCTCAGC	TGAAGTCTCT	CACACACTCC	350
CTCTCTCCCC	AGGCCTGTGG	GTCTCCATCG	CCCAGCTCCT	GCCCACGCTC	400
CTGACTGCTG	CCCTGACCAG	AGTCATC			427
ATG TCT CTC	GAG CAG AGG	AGT CCG CAC	TGC AAG CCT	GAT GAA	469
GAC CTT GAA	GCC CAA GGA	GAG GAC TTG	GGC CTG ATG	GGT GCA	511
CAG GAA CCC	ACA GGC GAG	GAG GAG GAG	ACT ACC TCC	TCC TCT	553
GAC AGC AAG	GAG GAG GAG	GTG TCT GCT	GCT GGG TCA	TCA AGT	595
CCT CCC CAG	AGT CCT CAG	GGA GGC GCT	TCC TCC TCC	ATT TCC	637
GTC TAC TAC	ACT TTA TGG	AGC CAA TTC	GAT GAG GGC	TCC AGC	679
AGT CAA GAA	GAG GAA GAG	CCA AGC TCC	TCG GTC GAC	CCA GCT	721
CAG CTG GAG	TTC ATG TTC	CAA GAA GCA	CTG AAA TTG	AAG GTG	763
GCT GAG TTG	GTT CAT TTC	CTG CTC CAC	AAA TAT CGA	GTC AAG	805
GAG CCG GTC	ACA AAG GCA	GAA ATG CTG	GAG AGC GTC	ATC AAA	847
AAT TAC AAG	CGC TAC TTT	CCT GTG ATC	TTC GGC AAA	GCC TCC	889
GAG TTC ATG	CAG GTG ATC	TTT GGC ACT	GAT GTG AAG	GAG GTG	931
GAC CCC GCC	GGC CAC TCC	TAC ATC CTT	GTC ACT GCT	CTT GGC	973
CTC TCG TGC	GAT AGC ATG	CTG GGT GAT	GGT CAT AGC	ATG CCC	1015
AAG GCC GCC	CTC CTG ATC	ATT GTC CTG	GGT GTG ATC	CTA ACC	1057
AAA GAC AAC	TGC GCC CCT	GAA GAG GTT	ATC TGG GAA	GCG TTG	1099
AGT GTG ATG	GGG GTG TAT	GTT GGG AAG	GAG CAC ATG	TTC TAC	1141
GGG GAG CCC	AGG AAG CTG	CTC ACC CAA	GAT TGG GTG	CAG GAA	1183
AAC TAC CTG	GAG TAC CGG	CAG GTG CCC	GGC AGT GAT	CCT GCG	1225
CAC TAC GAG	TTC CTG TGG	GGT TCC AAG	GCC CAC GCT	GAA ACC	1267
AGC TAT GAG	AAG GTC ATA	AAT TAT TTG	GTC ATG CTC	AAT GCA	1309
AGA GAG CCC	ATC TGC TAC	CCA TCC CTT	TAT GAA GAG	GTT TTG	1351
GGA GAG GAG	CAA GAG GGA	GTC TGA			1375
GCACCAGCCG	CAGCCGGGGC	CAAAGTTTGT	GGGGTCA		1412

- (2) INFORMATION FOR SEQUENCE ID NO: 22:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 920 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-10 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

ACCTGCTCCA	GGACAAAGTG	GACCCCACTG	CATCAGCTCC	ACCTACCCTA	50
CTGTCAGTCC	TGGAGCCTTG	GCCTCTGCCG	GCTGCATCCT	GAGGAGCCAT	100
CTCTCACTTC	CTTCTTCAGG	TTCTCAGGGG	ACAGGGAGAG	CAAGAGGTCA	150
AGAGCTGTGG	GACACCACAG	AGCAGCACTG	AAGGAGAAGA	CCTGTAAGTT	200
GGCCTTTGTT	AGAACCTCCA	GGGTGTGGTT	CTCAGCTGTG	GCCACTTACA	250
CCCTCCCTCT	CTCCCCAGGC	CTGTGGGTCC	CCATCGCCCA	AGTCCTGCCC	300
ACACTCCCAC	CTGCTACCCT	GATCAGAGTC	ATC		333
ATG CCT CGA	GCT CCA AAG	CGT CAG CGC	TGC ATG CCT	GAA GAA	375
GAT CTT CAA	TCC CAA AGT	GAG ACA CAG	GGC CTC GAG	GGT GCA	417
CAG GCT CCC	CTG GCT GTG	GAG GAG GAT	GCT TCA TCA	TCC ACT	459
TCC ACC AGC	TCC TCT TTT	CCA TCC TCT	TTT CCC TCC	TCC TCC	501
TCT TCC TCC	TCC TCC TCC	TGC TAT CCT	CTA ATA CCA	AGC ACC	543
CCA GAG GAG	GTT TCT GCT	GAT GAT GAG	ACA CCA AAT	CCT CCC	585
CAG AGT GCT	CAG ATA GCC	TGC TCC TCC	CCC TCG GTC	GTT GCT	627
TCC CTT CCA	TTA GAT CAA	TCT GAT GAG	GGC TCC AGC	AGC CAA	669
AAG GAG GAG	AGT CCA AGC	ACC CTA CAG	GTC CTG CCA	GAC AGT	711
GAG TCT TTA	CCC AGA AGT	GAG ATA GAT	GAA AAG GTG	ACT GAT	753
TTG GTG CAG	TTT CTG CTC	TTC AAG TAT	CAA ATG AAG	GAG CCG	795
ATC ACA AAG	GCA GAA ATA	CTG GAG AGT	GTC ATA AAA	AAT TAT	837
GAA GAC CAC	TTC CCT TTG	TTG TTT AGT	GAA GCC TCC	GAG TGC	879
ATG CTG CTG	GTC TTT GGC	ATT GAT GTA	AAG GAA GTG	GAT CC	920

009250" 41562560

- (2) INFORMATION FOR SEQUENCE ID NO: 23:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1107 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-11 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AGAGAACAGG CCAACCTGGA GGACAGGAGT CCCAGGAGAA CCCAGAGGAT 50
 CACTGGAGGA GAACAAGTGT AAGTAGGCCT TTGTTAGATT CTCCATGGTT 100
 CATATCTCAT CTGAGTCTGT TCTCACGCTC CCTCTCTCCC CAGGCTGTGG 150
 GGCCCCATCA CCCAGATATT TCCCACAGTT CGGCCTGCTG ACCTAACCAG 200
 AGTCATCATG CCTCTTGAGC AAAGAAGTCA GCACTGCAAG CCTGAGGAAG 250
 CCTTCAGGCC CAAGAAGAAG ACCTGGGCCT GGTGGGTGCA CAGGCTCTCC 300
 AAGCTGAGGA GCAGGAGGCT GCCTTCTTCT CCTCTACTCT GAATGTGGGC 350
 ACTCTAGAGG AGTTGCCTGC TGCTGAGTCA CCAAGTCCTC CCCAGAGTCC 400
 TCAGGAAGAG TCCTTCTCTC CCACTGCCAT GGATGCCATC TTTGGGAGCC 450
 TATCTGATGA GGGCTCTGGC AGCCAAGAAA AGGAGGGGCC AAGTACCTCG 500
 CCTGACCTGA TAGACCCTGA GTCCTTTTCC CAAGATATAC TACATGACAA 550
 GATAATTGAT TTGGTTTATT TATTCTCCGC AAGTATCGAG TCAAGGGGCT 600
 GATCACAAAG GCAGAA 616
 ATG CTG GGG AGT GTC ATC AAA AAT TAT GAG GAC TAC TTT CCT 658
 GAG ATA TTT AGG GAA GCC TCT GTA TGC ATG CAA CTG CTC TTT 700
 GGC ATT GAT GTG AAG GAA GTG GAC CCC ACT AGC CAC TCC TAT 742
 GTC CTT GTC ACC TCC CTC AAC CTC TCT TAT GAT GGC ATA CAG 784
 TGT AAT GAG CAG AGC ATG CCC AAG TCT GGC CTC CTG ATA ATA 826
 GTC CTG GGT GTA ATC TTC ATG GAG GGG AAC TGC ATC CCT GAA 868
 GAG GTT ATG TGG GAA GTC CTG AGC ATT ATG GGG GTG TAT GCT 910
 GGA AGG GAG CAC TTC CTC TTT GGG GAG CCC AAG AGG CTC CTT 952
 ACC CAA AAT TGG GTG CAG GAA AAG TAC CTG GTG TAC CGG CAG 994
 GTG CCC GGC ACT GAT CCT GCA TGC TAT GAG TTC CTG TGG GGT 1036
 CCA AGG GCC CAC GCT GAG ACC AGC AAG ATG AAA GTT CTT GAG 1078
 TAC ATA GCC AAT GCC AAT GGG AGG GAT CC 1107

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- (2) INFORMATION FOR SEQUENCE ID NO: 24:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2150 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: smage-I
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

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TCTGTCTGCA	TATGCCTCCA	CTTGTGTGTA	GCAGTCTCAA	ATGGATCTCT	50
CTCTACAGAC	CTCTGTCTGT	GTCTGGCACC	CTAAGTGGCT	TTGCATGGGC	100
ACAGGTTTCT	CCCCCTGCAT	GGAGCTTAAA	TAGATCTTTC	TCCACAGGCC	150
TATACCCCTG	CATTGTAAGT	TTAAGTGGCT	TTATGTGGAT	ACAGGTCTCT	200
GCCCTTGTAT	GCAGGCCTAA	GTTTTTCTGT	CTGCTTAACC	CCTCCAAGTG	250
AAGCTAGTGA	AAGATCTAAC	CCACTTTTGG	AAGTCTGAAA	CTAGACTTTT	300
ATGCAGTGGC	CTAACAAGTT	TTAATTTCTT	CCACAGGGTT	TGCAGAAAAG	350
AGCTTGATCC	ACGAGTTCAG	AAGTCCTGGT	ATGTTCCTAG	AAAG	394
ATG TTC TCC	TGG AAA GCT	TCA AAA GCC	AGG TCT CCA	TTA AGT	436
CCA AGG TAT	TCT CTA CCT	GGT AGT ACA	GAG GTA CTT	ACA GGT	478
TGT CAT TCT	TAT CCT TCC	AGA TTC CTG	TCT GCC AGC	TCT TTT	520
ACT TCA GCC	CTG AGC ACA	GTC AAC ATG	CCT AGG GGT	CAA AAG	565
AGT AAG ACC	CGC TCC CGT	GCA AAA CGA	CAG CAG TCA	CGC AGG	604
GAG GTT CCA	GTA GTT CAG	CCC ACT GCA	GAG GAA GCA	GGG TCT	646
TCT CCT GTT	GAC CAG AGT	GCT GGG TCC	AGC TTC CCT	GGT GGT	688
TCT GCT CCT	CAG GGT GTG	AAA ACC CCT	GGA TCT TTT	GGT GCA	730
GGT GTA TCC	TGC ACA GGC	TCT GGT ATA	GGT GGT AGA	AAT GCT	772
GCT GTC CTG	CCT GAT ACA	AAA AGT TCA	GAT GGC ACC	CAG GCA	814
GGG ACT TCC	ATT CAG CAC	ACA CTG AAA	GAT CCT ATC	ATG AGG	856
AAG GCT AGT	GTG CTG ATA	GAA TTC CTG	CTA GAT AAA	TTT AAG	898
ATG AAA GAA	GCA GTT ACA	AGG AGT GAA	ATG CTG GCA	GTA GTT	940
AAC AAG AAG	TAT AAG GAG	CAA TTC CCT	GAG ATC CTC	AGG AGA	982
ACT TCT GCA	CGC CTA GAA	TTA GTC TTT	GGT CTT GAG	TTG AAG	1024
GAA ATT GAT	CCC AGC ACT	CAT TCC TAT	TTG CTG GTA	GGC AAA	1066
CTG GGT CTT	TCC ACT GAG	GGA AGT TTG	AGT AGT AAC	TGG GGG	1108
TTG CCT AGG	ACA GGT CTC	CTA ATG TCT	GTC CTA GGT	GTG ATC	1150
TTC ATG AAG	GGT AAC CGT	GCC ACT GAG	CAA GAG GTC	TGG CAA	1192
TTT CTG CAT	GGA GTG GGG	GTA TAT GCT	GGG AAG AAG	CAC TTG	1234
ATC TTT GGC	GAG CCT GAG	GAG TTT ATA	AGA GAT GTA	GTG CGG	1276
GAA AAT TAC	CTG GAG TAC	CGC CAG GTA	CCT GGC AGT	GAT CCC	1314
CCA AGC TAT	GAG TTC CTG	TGG GGA CCC	AGA GCC CAT	GCT GAA	1360
ACA ACC AAG	ATG AAA GTC	CTG GAA GTT	TTA GCT AAA	GTC AAT	1402
GGC ACA GTC	CCT AGT GCC	TTC CCT AAT	CTC TAC CAG	TTG GCT	1444
CTT AGA GAT	CAG GCA GGA	GGG GTG CCA	AGA AGG AGA	GTT CAA	1486
GGC AAG GGT	GTT CAT TCC	AAG GCC CCA	TCC CAA AAG	TCC TCT	1528
AAC ATG TAG					1537
TTGAGTCTGT	TCTGTTGTGT	TTGAAAAACA	GTCAGGCTCC	TAATCAGTAG	1587
AGAGTTCATA	GCCTACCAGA	ACCAACATGC	ATCCATTCTT	GGCCTGTTAT	1637
ACATTAGTAG	AATGGAGGCT	ATTTTGTGTA	CTTTTCAAAT	GTTTGTTTAA	1687
CTAAACAGTG	CTTTTTGCCA	TGCTTCTTGT	TAACTGCATA	AAGAGGTAAC	1737
TGTCACCTGT	CAGATTAGGA	CTTGTTTTGT	TATTTGCAAC	AAACTGGAAA	1787
ACATTATTTT	GTTTTTACTA	AAACATTGTG	TAACATTGCA	TTGGAGAAGG	1837
GATTGTCATG	GCAATGTGAT	ATCATACAGT	GGTGAAACAA	CAGTGAAGTG	1887
GGAAAGTTTA	TATTGTTAAT	TTTGAAAATT	TTATGAGTGT	GATTGCTGTA	1937
TACTTTTTTC	TTTTTTGTAT	AATGCTAAGT	GAAATAAAGT	TGGATTTGAT	1987
GACTTTACTC	AAATTCATTA	GAAAGTAAAT	CGTAAAACTC	TATTACTTTA	2037
TTATTTTCTT	CAATTATGAA	TTAAGCATTG	GTTATCTGGA	AGTTTCTCCA	2087
GTAGCACAGG	ATCTAGTATG	AAATGTATCT	AGTATAGGCA	CTGACAGTGA	2137
GTTATCAGAG	TCT				2150

- (2) INFORMATION FOR SEQUENCE ID NO: 25:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2099 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: smage-II
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

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ACCTTATTGG	GTCTGTCTGC	ATATGCCTCC	ACTTGTGTGT	AGCAGTCTCA	50
AATGGATCTC	TCTCTACAGA	CCTCTGCTCG	TGTCTGGCAC	CCTAAGTGGC	100
TTTGCATGGG	CACAGGTTTC	TGCCCCTGCA	TGGAGCTTAA	ATAGATCTTT	150
CTCCACAGGC	CTATACCCCT	GCATTGTAAG	TTTAAGTGGC	TTTATGTGGA	200
TACAGGTCTC	TGCCCTTGTA	TGCAGGCCCTA	AGTTTTTCTG	TCTGCTTAGC	250
CCCTCCAAGT	GAAGCTAGTG	AAAGATCTAA	CCCACTTTTG	GAAGTCTGAA	300
ACTAGACTTT	TATGCAGTGG	CCTAACCAAGT	TTTAATTTCT	TCCACAGGGT	350
TTGCAGAAAA	GAGCTTGATC	CACGAGTTCG	GAAGTCCTGG	TATGTTCTTA	400
GAAAGATGTT	CTCCTGGAAA	GCTTCAAAAAG	CCAGGTCTCC	ATTAAGTCCA	450
AGGTATTCTC	TACCTGGTAG	TACAGAGGTA	CTTACAGGTT	GTCATTCTTA	500
TCTTTCCAGA	TTCCTGTCTG	CCAGCTCTTT	TACTTCAGCC	CTGAGCACAG	550
TCAACATGCC	TAGGGGTCAA	AAGAGTAAGA	CCCGCTCCCG	TGCAAAACGA	600
CAGCAGTCAC	GCAGGGAGGT	TCCAGTAGTT	CAGCCCACTG	CAGAGGAAGC	650
AGGGTCTTCT	CCTGTTGACC	AGAGTGCTGG	GTCCAGCTTC	CCTGGTGGTT	700
CTGCTCCTCA	GGGTGTGAAA	ACCCCTGGAT	CTTTTGGTGC	AGGTGTATCC	750
TGCACAGGCT	CTGGTATAGG	TGGTAGAAAT	GCTGCTGTCC	TGCCTGATAC	800
AAAAAGTTCA	GATGGCACCC	AGGCAGGGAC	TTCCATTTCAG	CACACACTGA	850
AAGATCCTAT	CATGAGGAAG	GCTAGTGTGC	TGATAGAATT	CCTGCTAGAT	900
AAGTTTAAGA	TGAAAGAAGC	AGTTACAAGG	AGTGAAATGC	TGGCAGTAGT	950
TAACAAGAAG	TATAAGGAGC	AATTCCCTGA	GATCCTCAGG	AGAACTTCTG	1000
CACGCCTAGA	ATTAGTCTTT	GGTCTTGAGT	TGAAGGAAAT	TGATCCCAGC	1050
ACTCATTCCT	ATTTGCTGGT	AGGCCAACTG	GGTCTTTCCA	CTGAGGGAAG	1100
TTTGAGTAGT	AACTGGGGGT	TGCCTAGGAC	AGGTCTCCTA	ATGTCTGTCC	1150
TAGGTGTGAT	CTTCATGAAG	GGTAACCGTG	CCACTGAGCA	AGAGGTCTGG	1200
CAATTTCTGC	ATGGAGTGGG	GGTATATGCT	GGGAAGAAGC	ACTTGATCTT	1250
TGGCGAGCCT	GAGGAGTTTA	TAAGAGATGT	AGTGCGGGAA	AATTACCTGG	1300
AGTACCGCCA	GGTACCTGGC	AGTGATCCCC	CAAGCTATGA	GTTCTGTGG	1350
GGACCCAGAG	CCCATGCTGA	AACAACCAAG	ATGAAAGTCC	TGGAAGTTTT	1400
AGCTAAAGTC	AATGGCACAG	TCCCTAGTGC	CTTCCCTAAT	CTCTACCAGT	1450
TGGCTCCTAG	AGATCAGGCA	GGAGGGGTGC	CAAGAAGGAG	AGTTCAAGGC	1500
AAGGGTGTTT	ATTTCAAGGC	CCCATCCCAA	AAGTCCTCTA	ACATGTAGTT	1550
GAGTCTGTTT	TGTTGTGTTT	GAAAAACAGT	CAGGCTCCTA	ATCAGTAGAG	1600
AGTTCATAGC	CTACCAGAAC	CAACATGCAT	CCATTCTTGG	CCTGTTATAC	1650
ATTAGTAGAA	TGGAGGCTAT	TTTTGTTACT	TTTCAAATGT	TTGTTTAACT	1700
AAACAGTGCT	TTTTGCCATG	CTTCTTGTTA	ACTGCATAAA	GAGGTAAGTG	1750
TCACTTGTC	GATTAGGACT	TGTTTTGTGA	TTTGCAACAA	ACTGGAAAAC	1800
ATTATTTTGT	TTTTACTAAA	ACATTGTGTA	ACATTGCATT	GGAGAAGGGA	1850
TTGTTCATGGC	AATGTGATAT	CATACAGTGG	TGAAACAACA	GTGAAGTGGG	1900
AAAGTTTATA	TTGTTAGTTT	TGAAAATTTT	ATGAGTGTGA	TTGCTGTATA	1950
CTTTTTTCTT	TTTTGTATAA	TGCTAAGTGA	AATAAAGTTG	GATTTGATGA	2000
CTTTACTCAA	ATTCATTAGA	AAGTAAATCA	TAAACTCTA	TTACTTTATT	2050
ATTTCTTCA	ATTATTAATT	AAGCATTGGT	TATCTGGAAG	TTTCTCCAG	2099

- (2) INFORMATION FOR SEQUENCE ID NO: 26:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acids
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Ala Asp Pro Thr Gly His Ser Tyr
5

005250.4562560